

GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 19, 2002, 07:56:52 ; Search time 48 Seconds  
(without alignments)  
2343.753 Million cell updates/sec

Title: US-09-807-459-2

Perfect score: 2359

Sequence: 1 MAPSDVGDYTKTLAASES.....DPSKALIRKSTEDNLLK 458

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued\_Patents\_NA.\*

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6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	826.5	35.0	1990	6	Patent No. 5171685-5
3	826.5	35.0	1990	6	Patent No. 5518916-5
4	120	5.1	3883	1	US-08-468-036-33
5	120	5.1	3883	1	US-08-376-843-33
6	120	5.1	3884	4	US-09-541-782-3
7	119.5	5.1	4766	5	PCT-US93-07261-10
8	111	4.7	3278	1	US-08-484-105-13
9	111	4.7	3278	1	US-08-484-106-13
10	108.5	4.6	7568	2	US-08-694-869-2
11	108.5	4.6	7568	3	US-09-349-546-2
12	105.5	4.5	1766	2	US-08-453-848-8

13	105.5	4.5	1766	4	US-09-169-027-8	Sequence 8, Appl1
14	104.5	4.4	4071	4	US-09-091-117-3	Sequence 3, Appl1
15	103.5	4.4	1407	3	US-08-688-988-7	Sequence 7, Appl1
16	101.5	4.3	2134	2	US-08-799-138-3	Sequence 3, Appl1
17	101.5	4.3	2134	4	US-09-392-362-3	Sequence 3, Appl1
18	100.5	4.3	2244	4	US-09-272-414-1	Sequence 1, Appl1
19	100	4.2	4467	1	US-08-565-907A-1	Sequence 1, Appl1
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25	99	4.2	7100	4	US-09-308-375-1	Sequence 1, Appl1
26	98.5	4.2	2007	2	US-08-743-637B-169	Sequence 169, App
27	98.5	4.2	2007	3	US-08-526-840B-169	Sequence 169, App
28	97.5	4.1	1829	3	US-08-688-988-9	Sequence 9, Appl1
29	97.5	4.1	3279	5	PCT-US93-03077-2	Sequence 2, Appl1
30	97.5	4.1	5361	4	US-08-973-462-2	Sequence 2, Appl1
31	97.5	4.1	6152	4	US-08-973-462-1	Sequence 1, Appl1
32	97	4.1	2211	2	US-08-799-138-5	Sequence 5, Appl1
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38	96.5	4.1	2612	2	US-08-463-483A-31	Sequence 31, Appl1
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40	96.5	4.1	2612	2	US-08-470-566B-31	Sequence 31, Appl1
41	96.5	4.1	2612	2	US-08-838-219B-3	Sequence 3, Appl1
42	96.5	4.1	2612	2	US-08-469-334-31	Sequence 31, Appl1
43	96.5	4.1	2612	3	US-09-300-529-31	Sequence 31, Appl1
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45	96.5	4.1	2612	3	US-09-233-752A-3	Sequence 3, Appl1

#### ALIGNMENTS

RESULT 1  
US-07-803-636A-1  
; Sequence 1, Application US/07803636A  
; Patent No. 5422428  
; GENERAL INFORMATION:  
; APPLICANT: MCGUIRE, TRAVIS C., TERRY F. MCELMAIN, LANCE E. PERRYMAN,  
; APPLICANT: WILLIAM C. DAVIS  
; TITLE OF INVENTION: IMMUNIZATION AGAINST BABESIOSIS USING  
; TITLE OF INVENTION: PURIFIED SURFACE ANTIGENS OF BABESIA BIGEMINA AND SIMILAR  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID R. SALIMANCHIK  
; STREET: 2421 NW 41ST STREET, SUITE A-1  
; CITY: GAINESVILLE  
; STATE: FLORIDA  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/803,636A  
; FILING DATE: 19911206  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SALIMANCHIK, DAVID R  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: WAA-059.C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:



US-09-807-459-2 (1-458) x 5171685-5 (1-1990)

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Qy	21	ValAspSerAlaIaIaAsnAlaThrMetIleAsnSerAspMetSerAspTyrLeuSerAla	40
Db	272	ATGACCTCCGGTGCCACATGCACAACTACATTCAGAGATATGAACATGTTTTGACGAT	331
Qy	41	ValSerAspAsnPhenAlaGluArgIleCysSerGlnValProLysGlySerAsnCysSer	60
Db	332	GGTCGTAGAGAGATGTGTAATGATGTTCTCTTAATGCTCTCGAGAGAGCTCCAAAGCTGCT	391
Qy	61	AlaSerValSerAlaTyrMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSer	80
Db	392	GAGGTACTTAAACATTTATGCTGACCGCTTGTAAGTACCGAGATGCTTTACGATTCACAT	451
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Db	452	GTCAAATATCCGTTGATCTCAAGAGTACCAACCTCTATCTCTCCAAACCCCTTACAGTGG	511
Qy	101	GlnAlaIaIaPhenIleLeuPheLysGlnSerAspAlaAsnProIaIaAsnSerThrGluLys	120
Db	512	GATCTCTCCGTTCCAGATTGTTCAAAGAGTGCATCCAAACCTCCCAAGACAGCTATAAA	571
Qy	121	ArgPheThrMetArgPheArgArgGlyLysAsnHisSerTyrPheHisAspLeuValPhe	140
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Db	812	CAAACTATGAGCTATCATCATCAGCTGGATGTTCTCGAAGATTTT---GAGAAAGGAGGC	868
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QY	3327	PhepshenLysGIUlleargAspProserLysAlaLeuLysGIUlysValSerAsnAsp	346
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QY	3387	GIUAsnLysIleGIyGInGIyThrValAspPhe-----	397
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QY	416	GIUAlaAspAspLeuphegIuAsnLysIleGIyGInGIyThrValAspPheIleAsnLys	435
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QY	455	Leu 455	
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Patent No. 5518916			
APPLICANT: MCELMAN, TERRY F.; MCGUIRE, TRAVIS C.; JASMER,			
DOUGLAS P.; REUKER, DAVID W.; GOF, WILL L.; STILLNER, DAVID			
TITLE OF INVENTION: CLONED BABESIA DNA			
NUMBER OF SEQUENCES: 7			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/08/342,480			
FILING DATE: 21-NOV-1994			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: 989, 616			
FILING DATE: 14-DEC-1992			
APPLICATION NUMBER: 504,461			
FILING DATE: 04-APR-1990			
APPLICATION NUMBER: 333,155			
FILING DATE: 04-APR-1989			
SEQ ID NO:5:			
LENGTH: 1990			
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QY 141 AsnLeuLeuGluLysAsnValThrArgAspAlaAspAlaThrAspIleGluAsnPheAla 160
Db 632 GCTCTGTTGAACAACAATGCTGCAAGAGAACGAACTACCGATGTTGAATATCTTGTTC 691
QY 161 SerArgTyrLeuTyrMetAlaThrLeuTyrTyrLysThrTyrThrAsnValAspGluPhe 180
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Db 812 CAATATGATGATGATCATCATCAGTGGAATGTTCTGAAAGATTTC--GAAGAAAGAGAC 868
QY 221 ValSerArgLeuGlnHisIleThrSerSerTyrLysAspTyrMetLysPheGlnIlePro 240
Db 869 ATCGAAGTATCTACTCAACCTTACTAGCAGCTACGAAGATTACATGTTGACCCAGATTCCA 928
QY 241 AlaLeuProLysPheAlaLysArgPheSerLeuMetValIleGlnArgLeuAlaThr 260
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QY 261 ValAlaGlyTyrValAspThrProTyrTyrLysTyrTyrMetLysLeuLysAsnPhe 280
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QY 292 ----- 292
Db 1109 AAAAATCTATGAAAGCCAAATGTTGCTGAGCCCACTAAAGTTTATGACAGACACTCAC 1168
QY 293 -----PheAsnLysGlnIleArgGluProSerLysAlaLeuLysGlu 306
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Db 1229 GAGGCTCTCTCAAGTACCAACACTTCTTCGATGGAACATTTGGCCAAACCCCAAGGAG 1288
QY 327 PhePheAsnLysGluIleArgAspProSerLysAlaLeuLysValSerAsnAsp 346
Db 1289 TTTTTCAGGAAAGCTCCCAAGCCACTAAACATTTCTTACAGAAACATCGCTCAACCA 1348
QY 347 AlaLysAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnGln 366
Db 1349 ACCAAGGAGTCTTTC--AGGAGGCTCTCTCAAGCCACTTAAGCACTTCTTACGCGAGAT 1405
QY 367 IleArgAspProSerLysAlaLeuLysValSerThrGlyAlaGluAspLeuPhe 386

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QY 387 GluAsnLysIleGlyGlnGlyThrValAspPhe----- 397
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QY 398 -----IleAsnAsnGluIleArgAspProSerLysAlaLeuIleArgLysValTyrThr 415
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QY 416 GluAlaAspAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnLys 435
Db 1586 GCGCCCAAGAAAT--TTCATTTCCGACCCCACTGAGAGGTAAGTACTTAAGCAGTTC 1642
QY 436 GluIleArgAspProSerLysAlaLeuIleArg--LysValSerThrGluAlaAspAsn 454
Db 1643 ACTGTTGCGCAACCTACCAAGAAATTCCTGAAGAGAGCTTTAGAAATCTTAAGACGCA 1702
QY 455 Leu 455
Db 1703 TTA 1705

RESULT 4
US-08-468-036-33
; Sequence 33, Application US/08468036
; Patent No. 5728806
; GENERAL INFORMATION:
; APPLICANT: Demaggio, Anthony J.
; TITLE OF INVENTION: Materials and Methods Relating to Proteins that
; TITLE OF INVENTION: Interact with Casein Kinase I
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,036
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/184,605
; FILING DATE: 21-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5728806and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/31784
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3883 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-468-036-33

Alignment Scores:
Pred. NO.: 0.000286 Length: 3883
Score: 120.00 Matches: 121
Percent Similarity: 34.75% Conservative: 92
Best Local Similarity: 19.74% Mismatches: 214

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Query Match: 5.09% Indels: 186  
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 US-09-807-459-2 (1-458) x US-08-468-036-33 (1-3883)

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 QY 24 AlaAlaAsnAlaIleMetIle-----AsnSerAspMetSer 35  
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 DB 1291 AGTTCAGAGAGTAATTCAGAGAACAGTCTCCAGGTCATTAATGATCTACACCTTAA 1350  
 QY 80 Ser-----LeuIysTyrProLeuGluAlaIysTyrGlnProLeuThrLeuProAspPro 97  
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 DB 1351 GCTGCTCTATTAGAAAAAGTTAAGAGACAAATTCACCTGCCAATATCCATCAACGACAG 1410  
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 QY 127 ArgArgGlyIysAsnHisSerTyrPheHisAspLeuVal----- 139  
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 DB 1591 ATGAGAGGGCTTAAACCTTATACAAAAGGCTTAAAGCAATAGCAAGTACGCCACTTAA 1650  
 QY 156 IleGluAsnPheAlaSerArg-----TyrLeuTyrMetAlaIleThrLeuTyrIleThr 173  
 : : : : : : : : : : :  
 DB 1651 ATGAACGATTTTTCAGATAGATCTCATACCATTTTACATCTTGTATAGAAGCAT 1710  
 QY 174 Tyr-----ThrAsn 176  
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 DB 1711 CAGGATGAACATTTAGATTTCCAAATGAAATCTTGCGATTAGCTGCTCAGAAAACT 1770  
 QY 177 ValAspGluPheGly-----AlaSerPhePheAsnIysLeu 188  
 : : : : : : : : : : :  
 DB 1771 ATCAACAGATTCGAGCATTAATCAACGTGCCAAGAAGCGTTCATCAACCAAGT 1830  
 QY 189 SerPheThrThrGly----- 193  
 ||| : : : : :  
 DB 1831 CTATTGACGTGGCGAGGGTCATAAAGCACTCTAGATAAAAAGCGCCATTTACCTTTC 1890  
 QY 194 -----LeuPheGlyTyrPheIleIysArgAla 202  
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 DB 1891 CGTGAATGGAATTAACCCGCTGCTTCAGATTCCTCGGGGGGTAATATGCAAAACCGCA 1950  
 QY 203 LeuIysGlnIleIleArgSerAsnLeuProLeuAspIleGlyThrGluHisSerValSer 222  
 ||| : : : : :  
 DB 1951 CTA-----ATTGCTACTATATCGCTCAAGGTAACTTCGAAGAACAACGTCAGAT 2001  
 QY 223 ArgLeuGlnHisIleThrSerSerTyrIysAspTyrMetAspThrGlnIleProAlaLeu 242  
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 DB 2002 ACATTAGAGTAT--GCTTCGAAGGCTAAACCAATTAAAGAACAG-----CCGCAACTG 2052

QY 243 ProIysPheAlaIysArgPheSerLeuMet-----Val 253  
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 DB 2053 GGTATTATTATATAGATATTTTGGTTAAAAATATATACATGGAATTCACCAAGATT 2112  
 QY 254 ValGlnArgLeuLeuAlaThrValAlaGly-----TyrValAspThrProTyr 270  
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 DB 2113 AAATCGAATTTACTCTCTCAAAAGTCCAAGAAGAAATATATATGAGCCACATCTACATC 2172  
 QY 271 LysLysTyrPheIleMetLeuIysAsnIleMetValAsnArgValPheIleProThrIys 290  
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 DB 2173 AAAAATTGAAACGATGATTTAGAAAGTTATPAAA--AATGAAGTT----- 2214  
 QY 291 LysPhePheAsnIysGluIleArgIleProSerLysAlaLeuLysGluIysValSerThr 310  
 : : : : : : : : : : :  
 DB 2215 -----CAAGATGTAAGACAGAAATTTGAAAGTTGACATCGAAAAATGCAATTG 2262  
 QY 311 AspThrLysAspLeuPheGluAsnIysIleGlyGlnGlyThrValAspPheAsnIys 330  
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 DB 2263 CTAGTAAAGATTAATTAATGAAAGTCAAA-----GAAACTATTCATCTCAAAATTCG 2313  
 QY 331 GluIleArgAspProSerLysAlaLeu-----LysGlu 341  
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 DB 2314 CAATATGAAATCATTTGAAAATCACTACATATTAAGGCAACACTAGATAACAGCAT 2373  
 QY 342 LysValSerAsnAspAlaLysAspLeuPheGluAsnIysIleGlyGlnGlyThr----- 359  
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 DB 2374 AAAACTGAATATGAATATCCAT--TTAATACCAAACTACAGAAAGTTGACTGAGTA 2430  
 QY 360 -----ValAspPhe----- 362  
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 DB 2431 ATGCAAAATGGCCCTCATGATATACAAAAAAGAGAACTGACCTTAATCAAAAGTTGAA 2490  
 QY 363 -----IleAsnAsnGluIleArgAspProSerLysAlaLeuIleArgLysValSerThr 380  
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 DB 2491 ATGCAATATTAATGAAATTAATAAATGAATCTACACTCTTTTCAATTAACACT 2550  
 QY 381 GlyAlaGluAsp-----LeuPheGluAsnIysIleGlyGlnGlyThrValAspPheIle 398  
 : : : : : : : : : : :  
 DB 2551 ATGCAACAGGAAGATTTCTTCAAGGACTAATATC--CAACCAATCTTATATGATAC 2607  
 QY 399 AsnAsnGluIleArgAspProSerLysAlaLeu----- 409  
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 DB 2608 AAAAATGAAGTACTGACTTATGAGAACCACTGCAAGAAAGCTGAACTAATGTACAA 2667  
 QY 410 -----IleArgLysValTyrThrGluAlaAspAspLeuPheGlu-----AsnLys 424  
 : : : : : : : : : : :  
 DB 2668 GACTGTGTGAAGAAATTTTAAACGAATCTCTAATTTCTCAATGTGTATTTGAGAA 2727  
 QY 425 IleGlyGlnGlyThrValAspPhe-----IleAsnLysGluIleArgAspProSerLys 442  
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 DB 2728 ATCGCATATATAGAGTATTTCCAAAAATTTTATATAAAATATATGCGGAGAT----- 2781  
 QY 443 AlaLeuIleArgLysValSerThrGluAlaAspAsnLeu 455  
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RESULT 5  
 US-08-376-843-33  
 ; Sequence 33, Application US/08376843  
 ; Patent No. 5846764  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Demaggio, Anthony J.  
 ; APPLICANT: Hoechst, Merl F.  
 ; TITLE OF INVENTION: Materials and Methods Relating to Proteins  
 ; NUMBER OF SEQUENCES: 53  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: United States of America  
 ; ZIP: 60606-6402

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: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/376,843
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/184,605
: FILING DATE: 21-JAN-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: No. 5846764and, Greta E.
: REGISTRATION NUMBER: 35,302
: REFERENCE/DOCKET NUMBER: 27866/31784
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312/474-6300
: TELEFAX: 312/474-0448
:
: INFORMATION FOR SEQ ID NO: 33:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3883 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
:
: US-08-376-843-33
:
: Alignment Scores:
: Pred. No.: 0.000286 Length: 3883
: Score: 120.00 Matches: 121
: Percent Similarity: 34.75% Conservative: 92
: Best Local Similarity: 19.74% Mismatches: 214
: Query Match: 5.09% Indels: 186
: Gaps: 29
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: US-09-807-459-2 (1-458) x US-08-376-843-33 (1-3883)
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: QY 4 SeraspSerValGlyAspValThrLysThrLeuLeuAlaAlaSerGluSerValAspSer 23
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: Db 1051 AGCGATGACGAGGAAATATACCGAGGCTCTTTGAGATTGTTGACACATTTGCACTA 1110
:
: QY 24 AlaAlaAsnAlaIyrMelle-----AsnSerAspMetSer 35
: |||: |||||: |||:
: Db 1111 CAACGAGACGATTCGTAAGTAAATGTTCTCATGTAACCTACACAGAAATTTGAG 1170
:
: QY 36 AspThrLeuSerAlaValSerAsp-----AsnPhenAla 46
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: Db 1171 GACCTCTTGACACGCAATAGCAACGCTCTAGTATACTGGCTTTGACGGCAATTTATG 1230
:
: QY 47 GluArgIleCysSerGlnValProLysGlySerAsnCysSerAlaSerValSerAlaTyr 66
: :|||: |||: |||: |||: |||: |||:
: Db 1231 AAAAATGAGAGATTGTTGCTTCAAGACACCAATAATATACACATGACAGAGTCTAGT 1290
:
: QY 67 MetSerArgCysAlaLysGlnAspCys-----LeuThrLeuGln 79
: |||||: |||||: |||||:
: Db 1291 AGTTCCAGAGCTAATTTCTAGGACACGTTCTCCGAGCATTAATGATCAACCTTAA 1350
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: QY 80 Ser-----LeuLysTyrProLeuGlnLysTyrGlnProLeuThrLeuProAspPro 97
: :|||: |||: |||: |||: |||: |||:
: Db 1351 GCTGCTCTATTAGAAAAGTTTAAGGACAAATCACATCCGCAATACCATCAAGCAACAG 1410
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: QY 98 TyrGlnLeuGlnLysAlaAlaPheIleLeuPheLysGluSerAspAlaAsnProAlaAsnSer 117
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: Db 1411 TATCAACAAACAGGAGCGAGTAATTCAGGAACAACCTCTCTCAACTGCGCTCTACC 1470
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: QY 118 ThrGlu-----LysArgPheThrMetArgPhe 126
: |||: |||: |||: |||:
: Db 1471 ACTAATTAATGCTTCTAGTAAACCAACACAAATAGCGTCAAGAAAGTTGATGGCTCCA 1530
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: QY 127 ArgArgGlyLysAsnHisSerTyrPheHisAspLeuVal----- 139
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Db 1531 AATGCAAACTAATGTTATATACATCCAGAAATTTGCAAGAAATTTACATTAACAATGCT 1590
:
: QY 140 -----PheAsnLeuLeuGlnLysAsnValThr---ArgAspAlaAspAlaThrAsp 155
: |||||: |||||: |||||: |||: |||: |||:
: Db 1591 ATGAGGGGCTTAACCTATTTCACAAAAGCTTTAAAGCTATAGCAAGTACGCTCCACTAAA 1650
:
: QY 156 IleGluAsnPhenAlaSerArg-----TyrLeuTyrMetAlaThrLeuTyrTyrLysThr 173
: :|||: |||: |||: |||: |||: |||:
: Db 1651 ATGAACGATTTTTCACAGATGATTCATACCATTTTATACATCACTTTGTATAGAGCAT 1710
:
: QY 174 Tyr-----ThrAsn 176
: |||: |||:
: Db 1711 CAGGATGACATATTAGAAATTTCCAAAATGAATCTTGATGATTAAGCTGTTCAGAAAAC 1770
:
: QY 177 ValAspGluPheGly-----AlaSerPheAsnLysLeu 188
: :|||: |||: |||: |||: |||: |||:
: Db 1771 ATCAACAGATCCGAGCATTAATATCAACGTGCCAAAGAGCTGGTTCAATCAACCAAAAGT 1830
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: QY 189 SerPheThrThrGly----- 193
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: Db 1831 CTATTGACGCTGGCAGGATCATAAACGCACTCGATATAAAGCGCCCATATACCTTTC 1890
:
: QY 194 -----LeuPheGlyTTPGlyIleLysArgAla 202
: |||: |||: |||: |||:
: Db 1891 CGTAGAATGAATTCACCCGCTCTTCAGATTCCTGGTGATATACGAAAACCGCA 1950
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: QY 203 LeuLysGlnIleIleArgSerAsnLeuProLeuAspIleGlyThrGlnHisSerValSer 222
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: Db 1951 CTA-----ATTGCTACATATCCGCTGCAAAAGTAATCTTGAAAGAAACCTGCAGT 2001
:
: QY 223 ArgLeuGlnHisIleThrSerSerTyrLysAspTyrMetAspThrGlnIleProAlaLeu 242
: |||||: |||: |||: |||: |||: |||:
: Db 2002 ACATTAGAGTAT---GCYTCAAGGCTTAAAAACATTAGAACAAG---CCCAACTG 2052
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: QY 243 ProLysPheAlaLysArgPheSerLeuMet-----Val 253
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: Db 2053 GGTTCATTTAATAGCAAGATTTTGTGTTAAATAATATATGAAATTTAGCAAAAGTT 2112
:
: QY 254 ValGlnArgLeuLeuAlaThrValAlaGly-----TyrValAspThrProTyr 270
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: Db 2113 AAATCCGATTTACTCTCTACAAAGACCAAGAGAAATATATGACCAAGATCACATAC 2172
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: QY 271 LysLysTyrPyrMetLysLeuLysAsnPhenMetValAsnArgValPheIleProThrLys 290
: |||: |||: |||: |||: |||: |||:
: Db 2173 AAAAATTTGAACAGTATTTGAAGATTATAAA---AATGAGTT----- 2214
:
: QY 291 LysPhePheAsnLysGluIleArgGluProSerLysAlaLeuLysGluLysValSerThr 310
: :|||: |||: |||: |||: |||: |||:
: Db 2215 -----CAAGATGTGAAAAGAAATTTGAAGTTTGACATCGAAAATAGCATTG 2262
:
: QY 311 AspThrLysAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheAsnLys 330
: |||||: |||: |||: |||: |||: |||:
: Db 2263 CTAGTAAAGATTAATTCAGTCAAAA-----GAACTATTCATCTCAAAATTTGC 2313
:
: QY 331 GluIleArgAspProSerLysAlaLeu-----LysGlu 341
: :|||: |||: |||: |||:
: Db 2314 CAATAGATATATTGAAACCTACCATGATCATTTAAGGCGACAACTGATTAACAGCAT 2373
:
: QY 342 LysValSerAsnAspAlaLysAspLeuPheGluAsnLysIleGlyGlnGlyThr----- 359
: |||: |||: |||: |||: |||: |||:
: Db 2374 AAACCTGAATTTGAATATTCGAT---TTTAATTAACAAATACAGAAAGTGCAGAGTA 2430
:
: QY 360 -----ValAspPhe----- 362
: |||: |||: |||: |||:
: Db 2431 ATGCAAATGGCCCTACATGATTACAAAAGAAAGAGAACTTGACTTAATCAAAAGTTTGA 2490
:
: QY 363 -----IleAsnAsnGluIleArgAspProSerLysAlaLeuIleArgValSerThr 380
: |||: |||: |||: |||: |||: |||:
: Db 2491 ATGCATATTACTAAAGAAATTAATAAATTGAATCTACACATGTTTTCATCAATTAACCT 2550
:
: QY 381 GlyAlaGluAsp-----LeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIle 398
: :|||: |||: |||: |||: |||: |||:
: Db 2551 ATGCACAGGAAAGATTTCTTCAAGAGCTAATATC---CAACCAATCTTGATATGATC 2607

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Oy	399	AsnAsnIleuLeaRgsAPProSerLySAlaLeu-----	409
Db	2608	AAAAATGAAGTACTGACCTTTATTGAAACCATGCACAAGAAAAGCTGAACATAATGTACAA	2667
Oy	410	-----lleaRgLySVaLYrThrGIuaLaSPpleuPheGLu-----	AsnLys 424
Db	2668	GACTGTGTGAAGAAATTTTAACCGAATCCCAAAATTCCTTAANGTGTATTATGAGAAA	2722
Oy	425	lleGIyngInglYthrValASpHe-----lleasNlySGluilearGspProSerLyS	442
Db	2728	ATCGACATTAATAAGAGATGATTTCCAAAAATTTTATAAATAATATGACCGAAMT-----	2781
Oy	443	AlAleuilearGlySVaLSerThrGIuaLaSPAsnLeu 455	
Db	2782	-----CTTCTCATATTATACGAAGAAATTAACACATG 2814	
 RESULT 6 US-09-541-782-3			
; Sequence 3, Application US/09541782			
; Patent No. 6284480			
; GENERAL INFORMATION:			
; APPLICANT: Nislow, Corey			
; APPLICANT: Sakowicz, Roman			
; APPLICANT: Berand, Christophe			
; TITLE OF INVENTION: Antifungal Assay			
; FILE REFERENCE: 1015			
; CURRENT APPLICATION NUMBER: US/09/541,782			
; CURRENT FILING DATE: 2000-04-03			
; NUMBER OF SEQ ID NOS: 10			
; SOFTWARE: Fastseq for Windows Version 4.0			
; SEQ ID NO 3			
; LENGTH: 3884			
; TYPE: DNA			
; ORGANISM: Saccharomyces cerevisiae			
US-09-541-782-3			
 Alignment Scores:			
Pred. NO.:	0.000287	Length:	3884
Score:	120.00	Matches:	121
Percent Similarity:	34.75%	Conservative:	92
Best Local Similarity:	19.74%	Mismatches:	214
Query Match:	5.09%	Indels:	186
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Db	1052	AGCCATCGACGAGAATTAATACCGAGGGCTTTTGAAGTTGTTCACACATTGGAACATA	1111
Oy	24	AlAlaAlaSnAlaryMetIle-----	AsnSerASPmetSer 35
Db	1112	CACAGACAGCATTACTGACGTAATAATGTTCCTATTGAACTCTACACAGAACGAATTTGAAG	1171
Oy	36	AspyrLeuSerAlaValSerasp-----	AsnPhenAla 46
Db	1172	GACCTCTTGACACCAATATACACAGCGCTCTAGTAATACGTGCTTGACGCCCAATTTATG	1231
Oy	47	GlUAurgleeCySSerGIuValIProLYSGlySerAsnCYSserAlaSerValSerAlatyr 66	
Db	1232	AAAAAATTGAGAGATTTTGGCTTCACAGACAGCAAATATATACACATGACAAAGTCTAGT	1291
Oy	67	MeSerArgCYsaLalysGIaSPcys-----	LeuThrLeuGIln 79
Db	1292	AGTTCCAGAGGATTAATCTAGACAGCTTCCTCCAGGCTCATTAATGATATTAACACCTAAA	1351
Oy	80	ser-----LeuLYSTyrProLeuGIuaLaLYSTyrGIaProLeuThrLeuProaspPro 97	
Db	1352	GCCTGCTCTATTAAAGAAAAGGTTTAGAGCAAAATCACTGCCGAATTCATTCACAGCAACAG	1411
Oy	98	TyrIlnLeuNGluAlaAlaPheilleuPheLYSGluSerASPalaSNProAlaasnSer 117	

Db	1412	TATCAACACACACGAGGAGTGAATTCACGAAACAACCTCTTCTCTAACCTGTGGCTTACC	1417
Qy	118	Thrglu-----LysrghetrpheIarph	126
Db	1472	ACTAATAATGCTTCTAGTAACACCAACACAAATAACGGGTCAAAAGATTGCGATGGCTCCA	1531
Qy	127	ArgatdgGlyLysasnHisSerTyrPhenHisAspLeuVal-----	139
Db	1532	AATGACCAACTAATGGTATATATGATCATCCAGAAATTTCCAGAAATTTCCATAACAATGCT	1591
Qy	140	-----PheasnLeuGlyLysAsnValThr---ArgAspIaAspIaThrAsp	155
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Qy	156	IleGluAsnPheIaSerArg-----TyrLeuTyrMetAlaThrLeuTyrTyrLysThr	173
Db	1652	ATGAACGATTTTTCACAGTACATACATTTTACATCAGCTTTTACATCAGCTTTGTATTAAGAAAGAT	1711
Qy	174	Tyr-----ThrAsn	176
Db	1712	CAGGATGACATATTAGAAATTTCCAAATGAAATCTTGATTTAGCTGGTTCAAGAAAC	1771
Qy	177	ValAspGluPheGly-----AlaSerPheheAsnLysLeu	188
Db	1772	ATCAACACAGATCCGAGAGCATTAATCAACATGCCAAGAAAGAGCTGGTTCAATCAACCAAGT	1831
Qy	189	SerPheThrThrGly-----	193
Db	1832	CTATTGACGCTGGGACAGGTCATTAACGCACCTGTAAGTATAAAGCGGCATTAACCTTC	1891
Qy	194	-----LeuPheGlyTrpGlyIleLysArgIa	202
Db	1892	CGTGATGAAATTAAGACCCGCTGCTCAAGATTTCCCTGGGTGATACGAAACCCGA	1951
Qy	203	LeuLysGlnIleIleArgSerAsnLeuProLeuAspIleGlyThrGluHisSerValSer	222
Db	1952	CTA-----ATTGGTACTATATACGCCGCAAGAGTAATCTTGAAACACGCGAGT	2002
Qy	223	ArgLeuGlnHisIleThrSerSerTyrLysAspTyrMetAspThrGlnIleProIaLeu	242
Db	2003	ACATTAGAGTAT---GCTTCGAAGGCTAAACAACTTATAGACACAG-----CCGCACATG	2053
Qy	243	ProLysPheAlaLysArgPheSerLeuMet-----Val	253
Db	2054	GGTTCATTTATATAAAGAGATTTTGGCTTAATAAATATACATGCAATTACCAAAAGATT	2113
Qy	254	ValGlnArgLeuLeuAlaThrValAlaGly-----TyrValAspThrProTrpTyr	270
Db	2114	AAATCCGATTTACTCTCTCAAAAGTCCAAAGAAAGAAATATATATGAGCCAAAGATCACTAC	2173
Qy	271	LysLysTrpTyrMetLysLeuLysAsnPheMetValAsnArgValPheIleProThrLys	290
Db	2174	AAAAATTTGAACAGCTGATTTAGAAAGTTTAA--AAAGAGT--	2215
Qy	291	LysPhePheAsnLysGluIleArgGluProSerLysAlaLeuLysGluLysValSerThr	310
Db	2216	-----CAAGATATGTAAGAGCAATTTGAAGAGTTTGACATCGAAATAATGATTTG	2265
Qy	311	AspThrLysAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheheAsnLys	330
Db	2264	CTAGTAAGAAGTAATATGCAAGTCAAA--GAAACATTTCAATCTCAAAATTTGC	2314
Qy	331	GluIleArgAspProSerLysAlaLeu-----LysGlu	341
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Qy	342	LysValSerAsnAspAlaLysAspLeuPheGluAsnLysIleGlyGlnGlyThr-----	359
Db	2375	AAAACGTGAATTTGAATAATTCGCAT---TTTAATATACAAACTACAGAAAGTTGACTAGGTA	2431
Qy	360	-----ValAspPhe-----	362
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OY 363 -----IleasnangluileargAspProSerLysAlaLeuIleArgLysValSerThr 380
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Db 2492 ATGATATTACTAAGAAATTAATAAATGAAATCTACACTGTTTACATTTAAACACT 2551
OY 381 G1yAlaGluAsp-----LeupheGluAsnLysIleGlyGlnGlyThrValAspPheIle 398
      :|||: ||| ||| ||| ||| :|||: |||
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OY 399 AsnAsnGluIleArgAspProSerLysAlaLeu----- 409
      |||||: ||| :|||: |||
Db 2609 AAAATAGAGTACTGACTCTTATGAGAACCTGCAAGAAAAAGCTGAATATATACAAA 2668
OY 410 -----IleArgLysValIlyrThrGluAlaAspAspLeupheGlu-----AsnLys 424
      :|||: ||| ||| ||| ||| :|||: |||
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OY 425 IlegLysGlnGlyThrValAspPhe-----IleAsnLysGluIleArgAspProSerLys 442
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Db 2729 ATGCACATTAATAGACGTAGATTCTCAAAAAATTTTATAAAATATAGCCGAGAAAT----- 2782
OY 443 AlaLeuIleArgLysValSerThrGluAlaAspAsnLeu 455
Db 2783 -----CTTCTGATATTAGCGAAGAAATATACACATG 2815

RESULT 7
PCT-US93-07261-10
: Sequence 10, Application PC/TUS9307261
: GENERAL INFORMATION:
: TITLE OF INVENTION: PFEIMP3 MALARIA ANTIGEN, ANALOGS, ANTIBODIES AND USES THEREOF
: NUMBER OF SEQUENCES: 23
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: John H. C. Blasdale
: STREET: One Giralda Farms
: CITY: Madison
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07940-1000
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Macintosh
: OPERATING SYSTEM: Macintosh 6.0.5
: SOFTWARE: Microsoft Word 5.1a
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/07261
: FILING DATE: 19930805
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/927,531
: FILING DATE: 07-AUG-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Blasdale, John H. C.
: REGISTRATION NUMBER: 31,895
: REFERENCE/DOCKET NUMBER: DX0288K
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 201-822-7398
: TELEFAX: 201-822-7039
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4766 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cdna to mRNA
: ORIGINAL SOURCE:
: ORGANISM: Plasmodium falciparum
: STRAIN: Malayan Camp
: IMMEDIATE SOURCE:
: CLONE: p2b1:p12-1
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 3..4766
: PCT-US93-07261-10

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Alignment Scores:
Pred. No.: 0.000464
Score: 119.50
Percent Similarity: 48.11%
Best Local Similarity: 31.35%
Query Match: 5.07%
DB: 5 Gaps: 14

US-09-807-459-2 (1-458) x PCT-US93-07261-10 (1-4766)

OY 294 AsnLysGluIleArg---GluProSerLysAlaLeuLysGluLysValSerThrAspThr 312
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Db 3135 AATTAAGATTATCGAATAATTAAGATCTGAAGATTAAAGAAATGCAAGATTAATAAT 3194
OY 313 LysAspLeupheGluAsnLysIleGlyGlnGly-----ThrValAspPheAsn 329
      |||||: ||| :|||: |||
Db 3195 AAAGATTA---CAAAATTAAGATCTGAAGATTAAAGAAATGCAAGATTAATAAT 3251
OY 330 LysGluIleArgAspPro---SerLysAlaLeuLysGluLysValSerAsnAspAlaLys 348
      |||||: ||| :|||: |||
Db 3252 AAAGATTACAAATTAAGATCTGAAGATTAAAGAAATGCAAGCAAAAAAATTAATA 3311
OY 349 AspLeupheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnAsnGluIleArg 368
      :|||: ||| ||| ||| ||| :|||: |||
Db 3312 GAATTA---CAAAATTAAGATCTGAAGATTAAAGAA---AATGCAAGATTAAATA 3362
OY 369 AspProSerLysAlaLeuIleArgLysValSerThrGluAlaGluAspLeupheGlu--- 387
      :|||: ||| ||| ||| ||| :|||: |||
Db 3363 -----AATTAAGATTATCGAATAATTAAGATCTGATGATTAAAGAAATGCAAGACTA 3416
OY 388 -----AsnLysIleGlyGlnGly-----ThrValAspPheIle 398
      ||||| ||| |||
Db 3417 AAAATTAAGATTATCGAATAATTAAGATCTGATGATTAAAGAAATGCAAGATTAAATA 3476
OY 399 AsnAsnGluIleArgAspPro---SerLysAlaLeuIleArgLysValIlyrThrGluAla 417
      ||| |||||: ||| :|||: |||
Db 3477 AATTAAGATTATCGAATAATTAAGATCTGAAGATTAAAGAAATGATATATACAAAT--- 3533
OY 418 AspAspLeupheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnLysGluIle 437
      :|||: ||| ||| ||| ||| :|||: |||
Db 3534 AATGATTAAAGATTATCGAATAT---CAAAATTAAGATTATCTAATTAAGAAACATG 3587
OY 438 ArgAspProSerLysAlaLeuIleArgLysValSerThrGluAlaAsp----- 453
      :|||: ||| ||| ||| ||| :|||: |||
Db 3588 AAA-----AATTAAGACATTTAAACAAAGATTTCTTAATAAGACATGAAATATAA 3641
OY 454 AsnLeuGluLys 458
Db 3642 GAATATTAAATATAA 3656

RESULT 8
US-08-484-105-13
: Sequence 13, Application US/08484105
: Patent No. 5589341
: GENERAL INFORMATION:
: APPLICANT: STILLMAN, Bruce
: APPLICANT: BELL, Stephen P
: APPLICANT: KOBAYASHI, Ryuji
: APPLICANT: RINE, Jasper
: APPLICANT: FOSS, Margit
: APPLICANT: MCNALLY, Francis J
: APPLICANT: LAURENSEN, Patricia
: APPLICANT: HERSKOWITZ, Ira
: APPLICANT: LI, Joachim J
: APPLICANT: GAVIN, Kimberly
: TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES
: NUMBER OF SEQUENCES: 24
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
: STREET: 4 Embarcadero Center, Suite 3400
: CITY: San Francisco
: STATE: California
: COUNTRY: USA

```



```

ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,105
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard Aton
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59032/DJB/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEX: 910 277299
INFORMATION FOR SEO ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 3278 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: Linear
MOLECULE TYPE: CDNA
OS-08-484-105-13

```

```

: APPLICANT: STILLMAN, Bruce
: APPLICANT: BELL, Stephen P
: APPLICANT: KOBAYASHI, Ryuji
: APPLICANT: RINE, Jasper
: APPLICANT: FOSS, Margit
: APPLICANT: MCNALLY, Francis J
: APPLICANT: LAURENSEN, Patricia
: APPLICANT: HERSKOWITZ, Ira
: APPLICANT: LI, Joachim J
: APPLICANT: GAVIN, Kimberly
: TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES
: NUMBER OF SEQUENCES: 24
: CORRESPONDENCE ADDRESS:
: ADDRESS: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
: STREET: 4 Embarcadero Center, Suite 3400
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-4187
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/484,106
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Osman Ph.D., Richard Aron
: REGISTRATION NUMBER: 36,627
: REFERENCE/DOCKET NUMBER: A-59032/DJB/RAO
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 494-8700
: TELEFAX: (415) 494-8771
: TELEX: 910 277299
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3278 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: US-08-484-106-13

Alignment Scores:
Pred. No.: 0.00283 Length: 3278
Score: 111.00 Matches: 98
Percent Similarity: 35.50% Conservative: 82
Best Local Similarity: 19.33% Mismatches: 199
Query Match: 4.71% Indels: 128
DB: 1 Gaps: 22

US-09-807-459-2 (1-458) x US-08-484-106-13 (1-3278)
QY 5 AsperValGlyaspValThrLysThrLeuLeuAlaAlaSerGluSerValAspSerAla 24
D 1214 GAAGTATATCATGATATGATCGATTTATCTGATATCAAGAAAGTAAAGACAGTTT 1273
QY 25 AAlaSnAlaTyrMetIleAsnSerAsp-----MetSerAspTyrLeuSerAlaValSer 42
D 1274 GCAAAACGATCTCTTCGACAGTGTGAGAGTTTGAAGATTACAGCTCTGACAGAAAG 1333
QY 43 AspaSnPheAlaGluArgIleCysSerGlnVal----- 53
D 1334 CTTCGATTTGATGACCTCCGACAGAAAGAGTATTAACCAAGATATACCATTT 1393
QY 54 ---ProLysGlySerAsnCysSerAlaSerValSerAlaTyrMetSer-----Arg 69
D 1394 TCACCAAGTAAATACACAGACATCCATTCGACGATCAGCAGATTCAATCTCTTAAGAG 1453
QY 70 CysAlaLysGlnAspCysLeuThrLeuGlnSerLeuLysTyrProLeuGlnAlaLysTyr 89
D 1454 TTCTTTAAGAAATATATAGTGGCGGTAAAGGATATCTCATTTTCCAAACGATAT 1513
QY 90 GlnProLeuThrLeuProAspProTyrGlnLeuGlnAlaIlePheIleLeuPheLysGlu 109
D 1514 AAGATCCGAAGATTCCTGACTTGAACAT-----ATTTCCAAAGCAT 1558
QY 110 SerAlaAsnProAlaAsnSerThrGluLysArgPheTyrPheLysArgPheArgGly 129
D 1559 AATAATGATTTGATATAGCTGATTAAGAGAGATTCAGAACAGTTTCTGCTAAAGC 1618
QY 130 LysAsnHisSerTyrPheHisAspLeuValPheAsnLeuLeuGlnLysAsnValThrArg 149
D 1619 AAAATGAGACTATTTTCTTAAGGTGAAGAACATTAAGTCAAGAAATAGCAAGAA 1678
QY 150 Asp---AlaAspAlaThrAspIleGluAsnPhe---AlaSerArgTyrLeuTyrMetAla 167
D 1679 GAAATGTCAAAAGCTGCTGATTTGCAAAATATATCTCCGCAAGAAATGAATTTGCA 1738
QY 1679 ThrLeuTyrTyrLysThrTyrThrAsnValAspGluPheGlyAlaSerPhePheAsnLys 187
D 1739 AGTATATACCTCTCCTTACAGTGCATTT---GAGCAGCAGCAGTACAGCAGTATTTAC 1795
QY 188 LeuSerPheThrThrGlyLeuPheGlyTyrPheGlyIleLysArgAlaLeuLysGlnIle 207
D 1796 ATTGCGGCGCGCCAGCGGT-----GATAAACTTGACGCTTCGAGAGTACGTT 1846
QY 208 ArgSerAsnLeuProLeuAspIleGlyThr-----GluHisSerValSerArgLeu 224
D 1847 AAG-----GATTTATGACATCTGCAGCAGCAAAAGAACTTCAGAGATTC 1891
QY 225 GlnHisIle-----ThrSerSerTyrLys----- 232
D 1892 CAATCATTTGAATCAATGATTTAAGATGTGCAAGCAAGTATGATTAAGAGTCTTT 1951
QY 233 -----AspTyrMetAspThr 237
D 1952 TGGCAAAAATATCTGAGAAAGCTTACATCTGAGCTGCCAGTCAAGATCTCTGGAGTTT 2011
QY 238 GlnIleProAlaLeuProLysPheAlaLysArgPheSerLeuMetValIleGlnArgLeu 257
D 2012 TATTTTAAACAAAGTCCAGCTACGAAAGAAAGCTCTATCGTGTATTGTGGATGACGTT 2071
QY 258 LeuAlaThrValAlaGlyTyrValAspThrProTyr---TyrLysLysTrp-----Tyr 274
D 2072 GATGATTAAGTACGAAAGCAAGCAAGATCTAATGTCAACTCTTTAATCGGCTACCTAT 2131
QY 275 MetLysLeuLysAsnPheMetVal-----AsnArgValPheIleProThrLysLys 291
D 2132 TCAAAATGCCAAACCTTATTTGTTAGCTGTGCAAAACACCTTAGATCTCCGAAAGCCAT 2191
QY 292 PhePheAsnLys----- 295
D 2192 CTGCTAACCAAGATTTGCTCCAGATTTGTTTACTACATTTATCTTACGTGTACAG 2251
QY 296 -----GluIleArg----- 298
D 2252 CATGAGAGCTTAGAACAAATCATCAATTTGAGACTTAATATTGACAGATCTAGTTTC 2311
QY 299 -----GluProSerLysAlaLeuLysGlnLysValSerThrAspThrLysAspLeuPhe 316
D 2312 TATGTGACCCGAGACAGGAGATTCTGATCATGATCTCTCCGATAGTACAGTACATA-- 2368
QY 317 GluAsnLysIleGlyGlnGlyThrValAspPhePheAsnLysGluIleArgAspProSer 336
D 2369 GAAACTGATGAAGAAGAAAGCAAGAAAGACTTCTTAC-----TAT 2410
QY 337 LysAlaLeuLysGlnLysValSerAsnAspAlaLysAspLeuPheGluAsnLysIleGly 356
D 2411 AAACGACTAAACCTTAGATTAATCTGATCCATTCGATTCATCAAGAAATATTCCT 2470
QY 357 GlnGlyThrValAspPheIleAsnAsnGlnLysIleArgAspProSerLysAlaLeuIleArg 376
D 2471 AGT-----GTCAGTGTGATGTGCGGAGACCTTTAAAGTGTGCAAAAGA 2515

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Qy      377  LysValSerThrInGlyAlaGluAspLeu-----PheGluAsnLysIle--- 39
          |||                               |||
Db      2516 GCGGTAGAAATATGCCGAAATGATTACTTAAAGAGCGTTAGATATAGCAGCTAGTCAAT 25
          |||                               |||
Qy      391  -----GlyGlnGlyThrValAspPheIleAsnAsnGluLe 40
          :::                               :::
Db      2576 TCCAAAAAAGATACTAGTACGCGCAATGCTACAGGAATGAAGAATTACAGAGTGTAGAAATT 26
          :::                               :::
Qy      403  ArgAspProSerLysAlaLeu 409
          :::                               :::
Db      2636 AAGCATATTATTACCAAGCATTA 2656
          :::                               :::

RESULT 10
US-08-694-869-2
; Sequence 2, Application US/08694869
; Patent No. 5994123
; GENERAL INFORMATION:
; APPLICANT: Olszewski, N.
; APPLICANT: Tzafrir, I.
; APPLICANT: Somers, D. A.
; APPLICANT: Lockhart, B.
; APPLICANT: Torbert, K.
; TITLE OF INVENTION: SUGARCANE BACILLIFORM VIRUS
; TITLE OF INVENTION: PROMOTER
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS#E: Schwegman, Lundberg, Moessner & Kluth, P.A.
; STREET: P.O. Box 2938
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/694, 869
; FILING DATE: 09-AUG-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moessner, Warren D
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 600.369US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-373-6900
; TELEFAX: 612-339-3061
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7568 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; US-08-694-869-2

Alignment Scores:
Pred. NO.: 0.0232 Length: 7568
Score: 108.50 Matches: 97
Percent Similarity: 34.95% Conservative: 69
Best Local Similarity: 20.42% Mismatches: 154
Query Match: 4.60% Indels: 155
DB: 2 Gaps: 24
US-09-807-459-2 (1-458) x US-08-694-869-2 (1-7568)
Qy      51  SerGlnValProLysGlySerAsnCysSerAlaSerValSerAlaTyrMetSerArgCys 70

```

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Db 2528 AGAGCAAGATGATGATCACTTCTCTCAACCGA-----AT 2563
Qy 374 uilearglyvalserthrngly-----AlaGluaspLeupheGluaspLys11 390
    :::: ||| ||||| ||::: ||::: ||:::
Db 2564 CTTATCAAGATCTCTACGACGCAAAAGATAGTGAGAGAAAGAAATTTTCCCGCAGAGA 2623
Qy 390 eglYgInglYthrValAspPheIleAsnAsn-----GluIleAr 403
    ||| ||||| ||::: ||::: ||:::
Db 2624 AGACCAAGATTATTTCTGTGGAAGAAACGTGAGAGCCCTACCTGCTGAATTTGA 2683
Qy 403 gAspProSerLysAlaLeuIleArgLysValIYThrGluAlaAspLeupheGluAs 423
    :::: ||| ||||| ||::: ||::: ||:::
Db 2664 AGAAGATGACCAAGCGCTAAGAGA-----CTTGACAACATCATGAAAC 2728
Qy 423 nLysIleGlyGInglYthrValAspPheIleAsnLysGluIleArgAspProSerLysAl 443
    ||::: ||::: ||::: ||::: ||::: ||:::
Db 2729 AAAAGTT-----GTTGTTCAAGAGATTGAAGCCATCCAGCC 2767
Qy 443 aLeuIleArgLysValSerThrGluAla-AspAsnLeuLeu 456
    :::: ||| ||||| ||::: ||::: ||:::
Db 2768 AGTTGAAGCTAAGATGATACAGCAACGATGATCATCTGCTA 2808

RESULT 11
US-09-349-546-2
: Sequence 2, Application US/09349546
: Patent No. 6093569
: GENERAL INFORMATION:
: APPLICANT: Olszewski, N.
: APPLICANT: Tzafrir, I.
: APPLICANT: Somers, D.A.
: APPLICANT: Lockhart, B.
: APPLICANT: Torbert, K.
: TITLE OF INVENTION: Sugarcane bacilliform virus promoter
: FILE REFERENCE: 600.369US2
: CURRENT APPLICATION NUMBER: US/09/349.546
: EARLIER FILING DATE: 1999-07-08
: EARLIER APPLICATION NUMBER: US 08/694,869
: EARLIER FILING DATE: 1996-08-09
: EARLIER APPLICATION NUMBER: PCT/IB97/01338
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2
: LENGTH: 7568
: TYPE: DNA
: ORGANISM: sugarcane bacilliform virus
US-09-349-546-2

Alignment Scores:
Pred. NO.: 0.0232 Length: 7568
Score: 108.50 Matches: 97
Percent Similarity: 34.95% Conservative: 69
Best Local Similarity: 20.42% Mismatches: 154
Query Match: 4.60% Indels: 155
DB: 3 Gaps: 24

US-09-807-459-2 (1-458) x US-09-349-546-2 (1-7568)
Qy 51 serGInValProLysGlySerAsnCySerAlaSerValSerAlaTyrMetSerArgCys 70
    ||::: ||| ||||| ||::: ||::: ||:::
Db 1646 TCAGAGATGCCAGGTCAAGCATGCTTTCT-----ACGGTTACTCTGAGAGACCC 1699
Qy 71 AlalysGlnasp-----CysLeuThrLeuGln-SerLeuLys 82
    :::: ||| ||||| ||::: ||::: ||:::
Db 1700 GAGAGAGAAGACCTGTGAGATGCTCATGACAGCTGATGTGAGATGACAGAGCATGAA 1759
Qy 82 s-----TyrProLeuGluAlaLysTyrGlnPro----- 91
    :::: ||| ||||| ||::: ||::: ||:::
Db 1760 GAAGAGACCAAGAGCTTTCCAGAGAAAGTCTGTATGGCCCAAGAACTGATGATATTC 1819
Qy 92 -----LeuThrLeuProAspProTyrGlnLe 100
    :::: ||| ||||| ||::: ||::: ||:::
Db 1820 TCACAAAGCTTTTCAAGGAGCTTACGACAGATATCTCTCTGATGATGACAAATCAGCT 1879

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Qy 100 uGluAlaAlaPheIleLeuPheLysGluSerAspAlaAsnProAlaAsnSerThrGly 120
    :::: ||| ||||| ||::: ||::: ||:::
Db 1880 TCATATGACCTTTATC-----AAGCAGGA 1903
Qy 120 sArgPheThrMetLarPheArgArgGlyLysAsnHisSerTyrPheHisAsp----- 137
    ||| ||||| ||::: ||::: ||:::
Db 1904 AACATTGACGAATTTGAGACAGCAGACTCCGG-----TATATTCATCCCGGATACT 1957
Qy 138 -----LeuValPhe 140
    :::: ||| ||||| ||::: ||::: ||:::
Db 1958 AGCTTAGAATACAGCCTCTGATCCAGACTGTCAGAGAAACGTTTTCATGTTT 2017
Qy 140 eAsnLeuGluLysAsnValThrArgAspAlaAspAlaThrAspIleGlu---AsnPh 159
    :::: ||| ||||| ||::: ||::: ||:::
Db 2018 CCGTACATCAGAGATTAACCCCAAGAGTACTTGACTGATGAAATTTGATCGACAA 2077
Qy 159 eAlaSerArgTyrLeuTyrMetAlaThrLeuTyrTyrIsthrTyrThrAsnValAspGl 179
    :::: ||| ||||| ||::: ||::: ||:::
Db 2078 AGGACCAAGATGCTATGTGATCAATAGCTTCATGACAAAGATMAAGAT----- 2129
Qy 179 uPheGlyLaserPheAsnLysLeuSerPheThrThr-----GlyLeuPheG1 196
    ||||| ||||| ||::: ||::: ||:::
Db 2130 -----TTCTTTATGATCATCCAGCTTACTGTAAGTGAAAGGTTATGAAGG 2176
Qy 196 YTrP---GlyIleLysArgAlaLeuLysGluIleLeuArgSerAsnLeuProLeuAspI1 215
    ||||| ||||| ||::: ||::: ||:::
Db 2177 TTGGCAAGGA-----GAGGCCAATTAACATTTGA-- 2207
Qy 215 eGlyThrGluHisSerValSerArgLeuGlnHisIleThrSerSerTyrLysAspTyrMe 235
    ||||| ||||| ||::: ||::: ||:::
Db 2208 -----AGTTGATTAAGTCAAGATGTGTCAAAATCAACCAATGTGTTCACATAT-- 2258
Qy 235 tAspThrGluIleProAlaLeuProLysPheAlaLysArgPheSerLeuMetValValG1 255
    :::: ||| ||||| ||::: ||::: ||:::
Db 2259 -----AAGTTGAAGAGAGCGCTCTTTATCAAGCAACAAAGTATMAAGCATTTGA 2311
Qy 255 nArgLeuLeuAlaThrValAlaGlyTyrValAspThrProTyrTyrLysTyrTyrMe 275
    :::: ||| ||||| ||::: ||::: ||:::
Db 2312 AGCCATAAAAAAGATGCAAGCGCATCAGAGAGAGAAATGGAAC----- 2357
Qy 275 tLysLeuLysAsnPheMetValAsnArgValPheIleProThrLysLysPhePheAsnLys 295
    :::: ||| ||||| ||::: ||::: ||:::
Db 2358 -----ATTGTCATCAAGCTA-----GA 2377
Qy 295 sGluIleArgLysProSerLysAlaLeuLysGluLysValSerThrAspThrLysAspLe 315
    :::: ||| ||||| ||::: ||::: ||:::
Db 2378 GGTACTCATGCACTTACC-----AAGTGCAAGACTACA----- 2411
Qy 315 uPheGluAsnLysIleGlyGlnGlyThrValAspPheAsnLysGluIleArgAspPr 335
    ||||| ||||| ||::: ||::: ||:::
Db 2412 ---GAAATATATGATGGCACACAAATCCTTCAGATTCACAAATTTTGAAGGTGCAGTTTC 2467
Qy 335 oSerLysAlaLeuLysGluLysValSerAsnAspAla---LysAspLeuPheGluAsnLys 354
    ||||| ||||| ||::: ||::: ||:::
Db 2468 TTCAAAGCCAGTAGAGCAACACTCAGATGATGAGCATATATGCGCTCTTTGAAGAAAGA 2527
Qy 354 sIleGlyGlnGlyThrValAspPheIleAsnAsnGluIleArgAspProSerLysAlaLe 374
    :::: ||| ||||| ||::: ||::: ||:::
Db 2528 AGAGCAAGAGATGATCATCACTTCTCAACCGA-----AT 2563
Qy 374 uilearglyvalserthrngly-----AlaGluaspLeupheGluaspLys11 390
    :::: ||| ||||| ||::: ||::: ||:::
Db 2564 CTTATCAAGATCTCTACGACGCAAAAGCTAGTGAGAGAAAGAAATTTTCCCGCAGAGA 2623
Qy 390 eglYgInglYthrValAspPheIleAsnAsn-----GluIleAr 403
    ||| ||||| ||::: ||::: ||:::
Db 2624 AGACCAAGATTATTTCTGTGATTTTCTTGAAAGAAACGTGAGAGCCCTACCTGCTGAATTTGA 2683
Qy 403 gAspProSerLysAlaLeuIleArgLysValIYThrGluAlaAspLeupheGluAs 423
    :::: ||| ||||| ||::: ||::: ||:::
Db 2684 AGAAGATGACCAAGCGCTAAGAGA-----CTTGAAACAACATCATGAAAC 2728

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01      Yy      423 nlysiilgclnglgyrhalasphelileasnlysgjuillearygasproserlysai 443
02      Db      2729 AAAAGTT-----GTTGTCAAGAGATTGAAGACCATCCAGCC 2767
03      Yy      443 aleuilearglysalserthrcluua'-Aspasndeuteu 456
04      Db      2768 AGTTCGAGCTPAGATGACTGCATCAAGCACTGGATCATCTGCTA 2808
05      RESULT 12
06      US-08-453-948-8
07      : Sequence 8, Application US/08453848
08      : Patent No. 5858368
09      : GENERAL INFORMATION:
10      : APPLICANT: Smith, Gale Eugene
11      : APPLICANT: Voivovitz, Franklin
12      : APPLICANT: Wilkinson, Bethanie Elident
13      : APPLICANT: Voznesensky, Andrei I.
14      : APPLICANT: Hackett, Craig Stanway
15      : TITLE OF INVENTION: A METHOD FOR PRODUCING INFLUENZA
16      : TITLE OF INVENTION: HEMAGGLUTININ MULTIVALENT VACCINES
17      : NUMBER OF SEQUENCES: 31
18      : CORRESPONDENCE ADDRESSES:
19      : ADDRESSEE: Patrea L. Pabst
20      : STREET: 2800 One Atlantic Center
21      : STREET: 1201 West Peachtree Street
22      : CITY: Atlanta
23      : STATE: GA
24      : COUNTRY: USA
25      : ZIP: 30309-3450
26      : COMPUTER READABLE FORM:
27      : MEDIUM TYPE: Floppy disk
28      : COMPUTER: IBM PC compatible
29      : OPERATING SYSTEM: PC-DOS/MS-DOS
30      : SOFTWARE: PatentIn Release #1.0, Version #1.25
31      : CURRENT APPLICATION DATA:
32      : APPLICATION NUMBER: US/08/453,848
33      : FILING DATE: 30-MAY-1995
34      : CLASSIFICATION: 435
35      : PRIOR APPLICATION DATA:
36      : APPLICATION NUMBER: 08/120,607
37      : FILING DATE: 13-SEPT-1993
38      : CLASSIFICATION: 435
39      : ATTORNEY/AGENT INFORMATION:
40      : NAME: Pabst, Patrea L.
41      : REGISTRATION NUMBER: 31,284
42      : REFERENCE/DOCKET NUMBER: MGS10ICIP
43      : TELECOMMUNICATION INFORMATION:
44      : TELEPHONE: (404)-873-8794
45      : TELEFAX: (404)-873-8795
46      : INFORMATION FOR SEQ ID NO: 8:
47      : SEQUENCE CHARACTERISTICS:
48      : LENGTH: 1766 base pairs
49      : TYPE: nucleic acid
50      : STRANDEDNESS: single
51      : TOPOLOGY: linear
52      : MOLECULE TYPE: DNA (genomic)
53      : HYPOTHEetical: NO
54      : ANTI-SENSE: NO
55      : ORIGINAL SOURCE:
56      : ORGANISM: Influenza virus
57      : INDIVIDUAL ISOLATE: A/Texas/36/91 rHA
58      : FEATURE:
59      : NAME/KEY: polyhedrin mRNA leader (partial)
60      : LOCATION: 1 to 18
61      : FEATURE:
62      : NAME/KEY: coding region for AcNPV 61k protein signal
63      : NAME/KEY: peptide
64      : LOCATION: 19 to 72
65      : FEATURE:
66      : NAME/KEY: SmaI restriction site
67      : LOCATION: 76 to 81
68      : FEATURE:
69      : NAME/KEY: KpnI restriction site

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[illegible]

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Db 1486 TTGAAATTCATGACAGTGTACCAATGAA-----TCGATGGAA 1524
Oy 377 LysValSerThrGlyAlaGluAspLeu-----PheGluAsnLysIleGlyGln 392
Db 1525 AGGTGTGAAAAATGGAAGTCTTGTGACTATCCAAATATTCGAAAGATCAAAAGTTAAACAGG 1564
Oy 393 GlyThrValAspPheIleAsnAsnGlu 401
Db 1585 GGAATAATGTGATGACGTGAATTTGAA 1611

RESULT 13
US-09-169-027-8
; Sequence 8, Application US/09169027
; Patent No. 6245532
; GENERAL INFORMATION:
; APPLICANT: Smith, Gale Eugene
; APPLICANT: Volnovitz, Franklin
; APPLICANT: Wilkinson, Bethanie Elident
; APPLICANT: Voznesensky, Andrei I.
; APPLICANT: Hackett, Craig Stanway
; TITLE OF INVENTION: A METHOD FOR PRODUCING INFLUENZA
; TITLE OF INVENTION: HEMAGGLUTININ MULTIVALENT VACCINES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/169,027
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/453,848
; FILING DATE: 30-MAY-1995
; APPLICATION NUMBER: 08/120,607
; FILING DATE: 13-SEPT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MGS101CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-873-8794
; TELEFAX: (404)-873-8795
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1766 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Influenza virus
; INDIVIDUAL ISOLATE: A/Texas/36/91 rHA
; FEATURE:
; NAME/KEY: polyhedrin mRNA leader (partial)
; LOCATION: 1 to 18
; NAME/KEY: coding region for AcNPV 61k protein signal
; NAME/KEY: peptide
; LOCATION: 19 to 72
; FEATURE:

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; NAME/KEY: SmaI restriction site
; LOCATION: 76 to 81
; FEATURE:
; NAME/KEY: KpnI restriction site
; LOCATION: 82 to 87
; FEATURE:
; NAME/KEY: SmaI restriction site
; LOCATION: 88 to 93
; FEATURE:
; NAME/KEY: coding region for mature rHA
; LOCATION: 73 to 1734
; FEATURE:
; NAME/KEY: KpnI restriction site
; LOCATION: 1744 to 1749
; FEATURE:
; NAME/KEY: BglII restriction site
; LOCATION: 1750 to 1755
; FEATURE:
; NAME/KEY: universal translation termination signal
; LOCATION: 1756 to 1766

US-09-169-027-8

Alignment Scores:
Pred. No.: 0.0049 length: 1766
Score: 105.50 Matches: 60
Percent Similarity: 36.068 Conservative: 37
Best Local Similarity: 22.308 Mismatches: 87
Query Match: 4.47% Indels: 85
DB: Gaps: 14

US-09-807-459-2 (1-458) x US-09-169-027-8 (1-1766)
Oy 195 PheGlyTrpGlyIleLysArgAlaLeuLysGlnIleIleArgSerAsnLeuProLeuAsp 214
Db 874 TTGTGGTCAGCA-----ATCATCACTCAACGATCAATGAT 912
Oy 215 IleGlyThrGluHisSerValSerArgLeuGlnHisIleThrSer-----TyrLys 232
Db 913 GAATGTGACGGCAAGTGTCAACACCCAGGAGCTATTAACAGTATCTCTTCCTCCAG 972
Oy 233 AspTyrMetAspThrGlnIleProAlaLeuProLysPheAlaLysArgPheSerLeuMet 252
Db 973 AATGTACACCCAGTCAACATATGAGAGTGTCCAAAGTATGTCAGAGTACNAATTAAGG 1032
Oy 253 ValVal-----GlnArgLeuLeuAlaThrVal 261
Db 1033 ATGTTACAGGACTTAAGAACATCCATTCATTCACAGAGGTTGTCAGCCATT 1092
Oy 262 AlaGlyTyrValAspThrProTyr-----TyrLysLysTrpTyr----- 274
Db 1093 GCCGGTTTCAITGAAAGGGGGGTGCACCTGCAATGATGATGATGATGATCATCAT 1152
Oy 275 -----MetLysLeuLysAsn 279
Db 1153 CAGAAATGAACAAGATCTGGCTATGTGCGGACCAAAAAGCACAAAATGCCATTAAAC 1212
Oy 280 PheMetValAsnArgVal-----PheIleProThr 289
Db 1213 GGGATTACAAACAAGGTGAATTCGTATGAGAAAATGAACACTCAATTCACAGCTGTG 1272
Oy 290 LysLysPhePheAsnLysGluIleArgGluProSerLysAlaLeuLysGluLysValSer 309
Db 1273 GGCAGAAAGATTCACACAAA---TTAGAAAAGAGATGCAAAACTTAATAAATAAGTTGAT 1329
Oy 310 ThrAspThrLysAsp-----LeuPheGluAsnLys 319
Db 1330 GATGATTTCTGCACATTGTCACATATATGACAGAAATGTGTCTTACTGGAATAAT--- 1366
Oy 320 IleGlyGlnGlyThrValAspPhePheAsnLysGluIleArgAspProSerLysAlaLeu 339
Db 1387 ---GGAAG---ACTTGGATTTCATGACATCAATGATGAAGAATCTGTATGACAAAAGTA 1440
Oy 340 LysGluLysValSerAsnAspAlaLysAspLeuPheGluAsnLysIleGlyGlnGlyThr 359

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Db 1441 AAAAGCAATGAGAAATATCCCAAGAA-----ATAGGGAACGGGTCT 1485
Oy 360 Valasphne-----Ileasnsgluileargasproserlysalaileuilearg 376
Db 1486 TTGTGAATCTATACAGACTGTAACAAATGA-----TGCATGGAA 1524
Oy 377 LysValSerThrGlyAlaGluAspLeu-----PheGluAsnLysIleGlyGln 392
Db 1525 AGTGGAAATATGCACTTATGACTATCCAAATATTCGGAAGAAATCAAGTTAAACAG 1584
Oy 393 GlyThrValAspPheIleAsnAsnGlu 401
Db 1585 GCAAAATTTGATGAGTGAATTTGAA 1611

RESULT 14
US-09-091-117-3
; Sequence 3, Application US/09091117
; Patent No. 6171589
; GENERAL INFORMATION:
; APPLICANT: The University of Melbourne
; TITLE OF INVENTION: Mycoplasma Recombinant Polypeptides and
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GREENLEE, WINNER and SULLIVAN P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: United States of America
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/091,117
; FILING DATE: 12 JUNE 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU96/00803
; FILING DATE: 13-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PN7127
; FILING DATE: 13-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: WINNER, Ellen P.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: +1 303 499 8080
; TELEFAX: +1 303 499 8089
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4071 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Mycoplasma pneumoniae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 250..654
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 762..3851
; OTHER INFORMATION: /codon= (seq: "tga" 3648..3651, aa: Trp)
; OTHER INFORMATION: /codon= (seq: "tga" 3663..3665, aa: Trp)
US-09-091-117-3

Alignment Scores:
Pred. NO.: 0.026 Length: 4071
Score: 104.50 Matches: 93
Percent Similarity: 36.67% Conservative: 68

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Best Local Similarity: 21.18% Mismatches: 173
Query Match: 4.43% Indels: 105
DB: 4 Gaps: 21

US-09-807-459-2 (1-458) x US-09-091-117-3 (1-4071)
Oy 78 LeuGlnSerIleuLysTyrProLeuGluAlaLysTyrGlnPro-----Leu 92
Db 912 CTTAATAGCTGTAAGTTGCA-----AAGACACACCGCTGCGGCAACTGAAAT 962
Oy 93 ThrIleuProAsp-----ProTyrGlnLeuGlu 101
Db 963 ACCGTGGAACGGAGCTGATTAATTAGTCACTATTAAGTCTCTACACAACTCTTT 1022
Oy 102 AlaAlaPheIleuPheLysGlu-----SerAsp 111
Db 1023 TTAGGGAAGAACCGCTTAAGATTAACCTCCAAAGTGAGTTGATTAATCTTAAGTAT 1082
Oy 112 AlaAsn-----ProAlaAsnSerThrGluLysArgPheTyrPheArgPheArgGly 129
Db 1083 GCGAAGGCCCTTCCAGCGCTTAACCGCTGATTTACAGAAATGGGTGACCAACAGCTGTT 1142
Oy 130 LysAsnHisSerTyrPheHisAspLeuValPheAsnLeuGluLysAsnValThrArg 149
Db 1143 AATCCAAACCAAGTTCTTTCATTTA-----AGTGGCCCAAGGTCAAACTTACCTT 1196
Oy 150 AspAlaAspAlaThrAspIleGluAsnPheAlaSerArgTyrLeuTyrMetAlaThrLeu 169
Db 1197 TCATCTGACAAAGGCTAGTTTACCTTATCTCCG----- 1235
Oy 170 TyrTyrLysThrTyrThrAsnValAspGluPheGlyAlaSerPheAsnLysLeuSer 189
Db 1236 -----TTACTTAC----- 1244
Oy 190 PheThrThrGlyLeuPheGlyTyrPheLysArgAlaLeuLysGlnIleLeuArgSer 209
Db 1245 TTCACCGAATCGCTCAGTGTGTAACAGTACCAAGAGTGTGCGTGTAGTGCATCC 1304
Oy 210 AsnLeuProLeuAspIleGlyThrGluHisSerValSerArgLeuGlnHisIleThrSer 229
Db 1305 AAACAAAGCTTGATTACTATGTCATGCTAGTCCCAAAATTTATGTTACCGCTG 1364
Oy 230 SerTyrLysAsp-----TyrMetAspThrGlnIleProAlaLeuPro 243
Db 1365 TCTTTACCAAGATTACACTTTGGCTTAACTATATGTTTGACCACTTACTTAAACGCT 1424
Oy 244 LysPheAlaLysArgPheSerLeuMetValValGlnArgLeuLeuAlaThrValaGly 263
Db 1425 AAGGTGTCAAATAAATTAGTTTAATCCGTCAAAAGCAATTTAAACCTGCC----- 1478
Oy 264 TyrValAspThrProTyrTyrLysTyrTyrTyrMetLysLeuLysAsnPheMetValAsn 283
Db 1479 -----TTTAGCAAGCTTTTACATGAGTGGGTGATGTGTTGACACAA 1520
Oy 284 ArgValPheIleProThrLysLysPhePheAsnLysGluIleArgGluProSerLysAla 303
Db 1521 AAGAAATTAGTAGTGAAGGTAATAATCACTCAACACCCAGCTGAAG-----GCTGAAGAC 1574
Oy 304 LeuLysGluLysValSerThrAspThrLysAspLeuPheGlu----- 317
Db 1575 GTAAGAAGAGGAGCTTAATGCCAATTAATAAACAATTTGACATTTGCCAAATATTGCT 1634
Oy 318 AsnLysIleGlyGlnGlyThrValAspPhePheAsnLysGluIleArgAspProSerLys 337
Db 1635 GAGCTAATGGGTGAAGCCCTTAAGAAATTTGGCAATCAACAAAGAAAGTCAACCATATTC 1694
Oy 338 AlaLeuLys-----GluLysValSerAsnAspAlaLysAspLeuPheGluAsnLysIle 355
Db 1695 TTCTTAAGGTAATGATTAAGCTTAAACAGAGTTTGGAAAACTTTT---AACTTATGTC 1751
Oy 356 GlyGlnGlyThrValAspPheIleAsnAsnGluIleArgAspProSerLysAlaLeuIle 375
Db 1752 CGTCTGATGGTGAATTTGTTAAGGCTTAATCCAAAGAGTATGTCAGCA----- 1805

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: SEQUENCE CHARACTERISTICS:
: LENGTH: 2134 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 127..1956
:
US-08-799-138-3

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Alignment Scores:	
Pred. No.:	0.021
Length:	2134
Matches:	68
Score:	101.50
Percent Similarity:	31.70%
Conservative:	67
Best Local Similarity:	17.48%
Mismatches:	127
Query Match:	4.30%
Indels:	127
DB:	2
Gaps:	17

US-09-807-459-2 (1-458) x US-08-799-138-3 (1-2134)

QY	139	ValPheasnleuLeuGluLysAsnValThrAspAlaAspAlaThrAspIleGluSn	158
Db	844	GTTCGTAATGATCACCACACAGCATTAACAGAAATGTTGACATGATTCGTAGCGCT	903
QY	159	PheAlaSerArgTyrLeuTyrMetAlaThrLeuTyrTyrLysThrTyrAsnValAsp	178
Db	904	AGAGAACGTGAGTAC---TTCATATGATCCCTCGAATATAAACACCTGGCAGAC-----	954
QY	179	GluPheGluLysaSerPhePheasnLysleuSerPheThrThhGlyLeuPheGlyTrrPoly	198
Db	955	AGAAATGGGTTCCAGACATCTGGCAGAGATG-----	984
QY	199	IleLysArgAlaLeuLysGlnIleIleArgSerAsnLeuProLeuAspIleIleThrGlu	218
Db	985	CTTCCAACAGCATTTGGACAGACATGAATCAATCAATCCAAATTCCT-----GGCATTCAA	10355
QY	219	HisSerValSerArg-----	223
Db	1036	TCCTTAATTAAACAAACAAATTCCTGAAGCTGAAGCTGAACCTAATCTGCTTTAGAAAGCT	10959
QY	224	-----LeuGlnHisIleThrSerSer-----	230
Db	1096	GTACGACCTGATGCTGGGGGAAAGTTGTATGCAATCATGAAATATGCGCCGTCATTTGAT	11555
QY	231	-----TyrLysAspTyrMet-----	235
Db	1156	CAAAATATTTAAAGACCATCTTGATGGCGGCGGCTCGAGGTCGATTAATTAATATGTC	12151
QY	236	---AspPheGlnIleProAlaLeuProLys-----PheAlaLysArgPheSerLeu	251
Db	1216	TTTGACAAATCAGCTCCCGCGTGTTTAAAAGTTGSCAATTTGATTAACAGCTTTCAATG	12757
QY	252	MetValValGlnArgLeuLeuAlaThrValAlaGlyTyr-----ValAspThrPro	268
Db	1276	GAAAATTAAGGAACCTTATTACTGGAAGCTGATGGGTATCACCTCATCATCTTATACCTCA	13359
QY	269	TrpTyrLysLysTrpTyrMetLysLys---LysAsnPheMetValAsnArgAlaPheIle	287
Db	1336	-----GACACAGAGATATCTCTCTTAATGAATCTTCTTAATACT-----	13777
QY	288	ProThrLysLysPhePheasnLysGluIleArgGluProSerLysAlaLeuLysGluLys	307
Db	1378	-----ATTAGGGCGCCGTCGAGAGCAGCTGTTATCGG	14110
QY	308	ValSerThrAspThrLysAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPhe	327
Db	1411	GTTCACGCTGTTAAAGGACTTGCTTCAC-----	1440
QY	328	PheasnLysGluIleArgAspProSerLysAlaLeuLysGluLysValSerAsnAspAla	347
Db	1441	-----AAAGCATATGTAACACTTTTGACATTTGAAGCAG	1473

Oy	348	LysaspLeuphegiuAsnIleuSilegIingIyThrValaspheileAsnsgIuile	367
Dd	1474	TATCTGTGCTCCGGGTGGAGGTTGGGGCGCTGCCTGTGATTCACTA---GAAAGATG	1530
Oy	368	ArgaspProSerIysalaleuIleargIysValSerThrclYalagIuaspLeuphegiu	387
Dd	1531	AGGGATGAAGCAAA-----AGAGCAACACTGCAGCTAGTGTAT	1566
Oy	388	AsnIysIleGIingIyThrValaspheileAsnsgIuIleArgaspProSerIys	407
Dd	1570	ATGAGAGTGCTGCTATTCAGACTGTGATTCTTTCGGAAAGCTTCCTCAAGATGCTGTAG	1623
Oy	408	Ala-----LeuIleargIysValIyThrclAlalaspaspLeuphegiuAsnIysIle	425
Dd	1630	GGTGCCAAATCCCAACACATTCAAATTTTGGATAGATATATGATTCAATATCTAAGCGCAATT	1685
Oy	426	GlyngIingIyThrValaspheileAsnIys-----	435
Dd	1690	GGAACCAAAATTTGTCATATGTCATATATGCTGTGCTCACTGCGGAATTCATTTCCC	1744
Oy	436	-----GluIleargaspProSerIysAlaleuIleargIysValSer	449
Dd	1750	AAGTCATCGTCTATTGTCAAGTGGCGGAGCAAAAGCAAGTCTCACTGATCACTTTT	1805
Oy	450	ThrGluIlaaspAsnleuLeuGluIys	458
Dd	1810	ACCGAGCTAGGCAAAATGAGACCAACG	1836

## RESULT

; Sequence 3, Application US/09392362

GENERAL INFORMATION:

TITLE OF INVENTION: PHRAGMOPLASTIN;  
NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:  
ADDRESS: CAREER UNIT - CRYSTAL  
; ADDRESS: CAREER UNIT - CRYSTAL

STREET: 800 SUPERIOR AVENUE  
CITY: CLEVELAND

STATE: OHIO  
COUNTRY: USA

ZIP: 44

Alignment Scores:	
Pred. No.:	0 021
Score:	101.50
Percent Similarity:	34.70%
Best Local Similarity:	17.48%
Query Match:	4.30%
DB:	4
Length:	2134
Matches:	68
Conservative:	67
Mismatches:	127
Indels:	127
Gaps:	17

US-09-807-459-2 (1-458) x US-09-392-362-3 (1-2134)

Oy	139	ValPheAsnLeuLeuGluLysAsnValThrArgAspAlaSerIleGluAsn	158
Dd	844	GTTGGAAATTAACATCACCAACAAGATAAACAAGATTGTGCATGATGCTCGTAGCCGT	9030
Oy	159	PheAlaSerArgTyrrLeuTyrrMetAlaThrLeuTyrrTyrrThrrTrpAsnValAsp	178
Dd	904	AGAGAACCCTGAAGTAC---TTCAAATAGTACCCCTGAAATATTAACACCTTGCGAAC----	954
Oy	179	GluProGlyAlaSerPhePheAsnLysLeuSerPheThrGlyLeuPheGlyTrpGly	198
Dd	955	AGAAATGGCTTCGAGCATCTGCCGAAAGTg-----	984
Oy	199	IleLysArgAlaLeuLysGlnIleIleArgSerAsnLeuProLeuAspIleGlyThrGlu	218
Dd	965	CTCTCAAGCATTGTGGAGACAGTATCATGTCAAAATTCTCT-----GGCATTCAA	1030
Oy	219	HISerValSerArg-----	223
Dd	1036	TCTCTAATTAAACAAAACAAATTGTGTAAGCTGAACCTGAACCTGAACCTGTTAGAAAACTT	109
Oy	224	-----LeuGlnHisIleThrSerSer-----	230
Dd	1096	GTACGAGCTGATGCTGGGGAAAGTTGTATGCATCATGGAATATATCCGCTCATTTTGAT	115
Oy	231	-----TyrrAspTyrrMet-----	235
Dd	1156	CAAAATTTTAAAGACATCTTGATGGCGTGGCGCTCGAGTGATATAAAATTTATAAGTCT	121
Oy	236	---AspThrGlnIleProAlaLeuProLys-----PheAlaLysArgPheSerLeu	251
Dd	1216	TTTTGCATTCAGCTCCCCGCTGCTTTAAAAAGGTTCGACGTTGATAGCAGCTTTCATG	127
Oy	252	MetValValGlnArgLeuLeuAlaThrValAlaGlyYr-----ValAspThrPro	268
Dd	1276	GAAAATATAAGAAACTTATTACTGAAAGCTGATGGGTATCAGCCTCATCTTATAGCTCA	133
Oy	269	TryPtyrLysTrpTyrrMetLysLeu---LysAsnHemetyAlaAsnArgValPheIle	287
Dd	1336	-----GAACAAGATATACGCGCTTAATGAATCTTCTCAATAACT-----	137
Oy	288	ProThrLysLysPhePheAsnLysGluIleArgGluProSerLysAlaLeuLysGluLys	307
Dd	1378	-----ATTAAGGGCCCTCTGAGCGACGCTGTGATGCG	141
Oy	308	ValSerThrAspThrLysAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPhe	327
Dd	1411	GTTCACTGCGCTTAAAGACATTGCTCAC-----	144
Oy	328	PheAsnLysGluIleArgAspProSerLysAlaLeuLysGluLysValSerAsnAspAla	347
Dd	1441	-----AAAGCTATCATGAGACTTTGGACTTGAAGCAG	147
Oy	348	LysAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnAsnGluIle	367
Dd	1474	TATCTGTGCTTCGCGGTTGAGAGTTGGGGCTGCTGCTGTATATTCACAA-----GAAAGATG	153
Oy	368	ArgAspProSerLysAlaLeuIleArgLysValSerThrGlyAlaGluAspLeuPheGlu	387
Dd	1531	AGGATGAAACCAA-----AGACCAACACTGCAGCTAGATTGAT	156
Oy	388	AsnLysIleGlyGlnGlyThrValAspPheIleAsnAsnGluIleArgAspProSerLys	407

Db	1570	ATGCAAGTGGCTATCTGACTGTTGATTTCTTTCCGAACTTCCTCCACAGTCTGTATAG	1629
Qy	408	Ala-----LeuIleargLysValIYrThrGluAlaAspAspLeuPheGluAsnLysIle	425
Db	1630	GGTGGCAATCCCAACACATTCAAATTTTGTATGATATATATGATTCATATCTAAGCGCAATT	1689
Qy	426	GlyGlnGlyThrValAspPheIleAsnLys-----	435
Db	1690	GGAAACACAAATTTGTCAATATGTCAAATATGCTGTGCTACACGTGGGAATTCATTC	1749
Qy	436	-----GuileIargAspProSerLysAlaLeuIleargLysValSer	449
Db	1750	AAGTCATCCGCTCTTGTGTCAAGTCGGGAGGCAAAAGCAAGTCTACTGTATCATTTT	1809
Qy	450	ThrGluAlaAspAsnLeuGluLys 458	
Db	1810	ACCGAGTAAAGCAAAATGAGACCAAG 1836	
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; Sequence 1, Application US/09272414A			
; Patent No. 6238885			
; GENERAL INFORMATION:			
; APPLICANT: Wallis, Nicola G.			
; TITLE OF INVENTION: Histidine kinase			
; FILE REFERENCE: GMI0202			
; CURRENT APPLICATION NUMBER: US/09/272,414A			
; CURRENT FILING DATE: 1999-03-19			
; NUMBER OF SEQ ID NOS: 2			
; SOFTWARE: PasteSeq for Windows Version 4.0			
; SEQ ID NO 1			
; LENGTH: 2244			
; TYPE: DNA			
; ORGANISM: Staphylococcus aureus			
US-09-272-414-1			
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Pred. No.: 0.0304 Length: 2244			
Score: 100.50 Matches: 101			
Percent Similarity: 35.26% Conservative: 70			
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Query Match: 4.26% Indels: 156			
DB: 4 Gaps: 22			
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Db	191	GCATACATTTTCACACAGAAACCGAAATATG-----	223
Qy	60	SerAlaSerValSerAlaCatalYrMetSerArgCys-AlaLysGlnAspCysLeuThrLeuG	79
Db	224	-----CATTAAGACAGATGCTGAACATAAGTCACTACGTGCGAACA	265
Qy	79	nSerIleuLysTyrProLeuGluAlaLysTyrGlnProLeuThrLeuProAspProTyrG	99
Db	266	ATTCACATTAATAAGACAGACCAATTAATAATTTAGTCAAACTTAATTAAGAAATCCGTGG	325
Qy	99	nLeuGluAlaIlePheIleuPheLysGluSerAspAlaAsnProAlaAsnSerThrG	119
Db	326	GTTGATGATTTAATAATAAATCAATGCTCAATCAACGGCTTCACTTTCTAATATTAATAA	385
Qy	119	uLysArgPheThrPheLysArgPheArgGlyLysAsnHisSerTyrPheHisAspLeuVa	139
Db	386	GCAA-----ATGTTGAATGAAGTAGTCACACAGCAACATTTTGAAGAT--GT	430
Qy	139	lPheAsnLeuLeuGluLysAsnValThrArgAspAlaAspAlaThrAspIleGluAsnPh	159
Db	431	GTTTGAT--AAAGGTAAATCTGTCTGCAAT-----GTAACGATTTAAAGAAA	478

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OY 159 ealaserargtyrleutyrmethylthrleutyrrylsthrtyrthrasnvalaspel 179
DB 479 GGGTTCATCTCAACAATATAATT--TTGTTAGCTATCCACAAAAGCAGACAG-- 530
OY 179 ubheglalasrphheasnlylseuserpetherthrthrglyleuphgltyrplcylil 199
DB 531 -----AATAGTCATAGCAAAATATATACGAGCTTT-----AT 562
OY 199 elysaralaleulysglnilleleargserasnleuproleuasplileglythrcluhl 219
DB 563 ATATAAGACTTGAAATCAATCAAGATACAAAT-----AA 598
OY 219 sservalaserargleuglnihislerhserserlyrlylsasptyrmetaspthrclnil 239
DB 599 TCGTATTAGATATACATATATATACGGCT----- 629
OY 239 eproalaleuprolysphlealalysargheserleuemetvalvalglargleuual 259
DB 630 -----GTTATTCTTCAACAAATTAC 649
OY 259 aathrvalalaglyrvalasprthprotrpyrlylsystpyrmetelysleulysas 279
DB 650 AACAGCTCTTGGCTT----- 665
OY 279 nphemetvalasnargvalphelleprothrlyslsyphepheasnlysglnileargel 299
DB 666 -TTCTTATCGTACAGAAATTAACAACCTTTAAAGCGTTAAAGACCAAGTACAGCTGT 724
OY 299 ubroserlysalaleulysglnilysvalserthrapsrthlylsaspleuphegluasny 319
DB 725 ATCTGAAGGGATTACTCTTATATAACCTCTGTGCACAAAGAAAGT-----GA 772
OY 319 slileglynglythrvalasphpe-----pheasnlysglnileargasproserly 337
DB 773 AATTGGTCATATTGACAGCATTTAATCAGATGACGAAATCGAAGAGCATGCTCGA 832
OY 337 salaleulysglnilysvalserasnspalalysaspleuphegluaslyslilegly 357
DB 833 CCCATTA-----TCCACATCTTAATAATATTAGACACGCTTAANTACTTATGGTAGA 886
OY 357 nglythrval-----As 361
DB 887 AGGTGCTCAGTAATTAATGAGAGTCGACAAATTATCTTATATAGATGGCGATGA 946
OY 361 pphelleasnangluileargasproserlysalaleulilearglylsvalserthrgl 381
DB 947 TATTATGGCAATATTGATGAGATGCTAAAGCTTCTTATTAAAGCAAAAT----- 998
OY 381 yalagluaspleuphegluaslyslileglynglythrvalasphheileasnangl 401
DB 999 -----GAAAGTACTTTTAAATCAAAA-----CAAACGGA 1027
OY 401 ulileargasp-----Proserlysalaleulileargly 412
DB 1028 AATGCGTGATTTAGAAATGATGACGATCTTTGTTGTGGACCAACAAGTATATCATATA 1087
OY 412 s-----Valtyrthrghualasaspaspleuphegluas 423
DB 1088 GATTGAACAGGAGTAAGAGTGTGTGTGGACAGTTCGATGATGACTAATAGCA 1147
OY 423 nlyslileglynglythrvalasphhele-----Asnlysglnileargaspr 440
DB 1148 CAATCTAGATCAAAATGACAAAGATTTCAATGATATCATGCAATTAATCGAACCACC 1207
OY 440 o-----Serlysalaleulilearglylsvalserthrghlualas 453
DB 1208 TATATCATTTACTACAAGTTTATATAGTCAATTTGATGATGATGTTACAGAACCGGA 1267
OY 453 pasnleuleuglu 457
DB 1268 TGAATAATAAAGAA 1280

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RESULT 19
US-08-565-907A-1
; Sequence 1, Application US/08565907A
; Patent No. 5814499
; GENERAL INFORMATION:
; APPLICANT: SYLVAIN MOINEAU, Barbara
; APPLICANT: J. Holler, Peter A. Vandenbergh,
; APPLICANT: Ebenezer R. Vedamuthu, Jeffrey K.
; APPLICANT: Kondo
; TITLE OF INVENTION: DNA Encoding Phage
; TITLE OF INVENTION: Abortive Infection Protein
; TITLE OF INVENTION: From Lactococcus
; TITLE OF INVENTION: Lactis, and Method of Use Thereof
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ian C. McLeod
; STREET: 2190 Commons Parkway
; CITY: Okemos
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48864
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 5.25 inch,
; MEDIUM TYPE: 360 Kb storage
; COMPUTER: Acer
; OPERATING SYSTEM: MS-DOS (version 4)
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/565,907A
; FILING DATE: December 1, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ian C. McLeod
; REGISTRATION NUMBER: 20,931
; REFERENCE/DOCKET NUMBER: Quest 4.1-152
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 347-4100
; TELEFAX: (517) 347-4103
; TELEX: No. 5814499e
; INFORMATION FOR SEO ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4467
; TYPE: Nucleotide
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE:
; DESCRIPTION: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N/A
; ORIGINAL SOURCE:
; ORGANISM: Lactococcus lactis
; STRAIN:
; INDIVIDUAL ISOLATE: w1
; DEVELOPMENTAL STAGE: N/A
; HAPLOTYPE: N/A
; TISSUE TYPE: N/A
; CELL TYPE: bacterium
; CELL LINE: N/A
; ORGANELLE: N/A
; IMMEDIATE SOURCE:
; LIBRARY: genomic
; CLONE: SMO-20
; POSITION IN GENOME: N/A
; FEATURE:
; NAME/KEY: phage abortive infection
; LOCATION: N/A
; IDENTIFICATION METHOD: sequencing
; OTHER INFORMATION: DNA encoding phage
; OTHER INFORMATION: resistance

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; PUBLICATION INFORMATION: N/A
US-08-565-907A-1

Alignment Scores:
Pred. No.: 0.11 Length: 4467
Score: 100.00 Matches: 96
Percent Similarity: 31.948 Conservative: 57
Best Local Similarity: 20.048 Mismatches: 121
Query Match: 4.24% Indels: 206
DB: 1 Gaps: 23

US-09-807-459-2 (1-458) x US-08-565-907A-1 (1-4467)

QY 129 GlyLysAsnHisSerTyrPhe----- 135
    |||||: |||||:
    1411 GGAAATCAGATCTCTTTTAACTAATTAATGAAATCCTTGACAGATTATTA 1470

QY 136 -----HisAspLeuValPheAsnLeuLeuGluys----- 145
    |||||: |||||:
    1471 AGAGCTCATGATTTTAAACACATTTTAAGCTTAAACCTATCAACAGACCCAGTA 1530

QY 146 -----AsnValThrArgAspAlaAspAlaThrAspIleGluAsnPheAlaSerArgTyr 163
    |||||: |||||: |||||:
    1531 TATTTTATATTTCCAAAAATATAGACCTAGACACATATAGATCCCAATTATATAC 1590

QY 164 LeuTyrMetAlaThrLeuTyrTyr-----LysThrTyrThrAsnVal--- 177
    |||||: |||||: |||||:
    1591 AGTATATATGCGATTAAATATATATATATGTCAGATTAAGAGTTATATGAACTATTT 1650

QY 178 -----AspGluPheGlyAlaSer---PhePheAsnLysLeuSerPhe----- 190
    |||||: |||||: |||||: |||||:
    1651 ATGTATACAAATTTTCAACCTCAAAATTTTAACTGAATTTGATTATTCCTAAG 1710

QY 191 -----ThrThrGlyLeuPheGlyTyrGlyIleLysArgAlaLeuLysGln 205
    |||||: |||||: |||||: |||||:
    1711 ACACAGAAATTACCAACAACTTATATATGCA---GCAATTAAGAA--- 1755

QY 206 IleIleArgSerAsnLeuProLeuAspIleGlyThr-----GluHis 219
    |||||: |||||: |||||: |||||:
    1756 -----TTTCACTTATGATTTATCTAATTTTATCATACCTTATATACAT 1800

QY 220 SerVal-----SerArgLeuGlnHisIleThrSerSerTyr 231
    |||||: |||||: |||||: |||||:
    1801 AGTATACCATGATGATTTGATGAGAAATCTGCATCTAACAACAAATGAAAAAGGCTT 1860

QY 232 LysAspTyrMetAspThrGlnIleProAlaLeuProLysPhe-AlaLysArgPheSerLe 251
    |||||: |||||: |||||: |||||:
    1861 TCTAATACATTAAGATACCTTGATTACAGCTGT---CAATACGACGAAACACATGCGAFT 1917

QY 251 uMetValValGlnArgLeuLeuAlaThrValAlaGlyTyrValAspThrProTyrTyr 271
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    1918 CCAACTGGAATCTATTTCTAGATTTATACCGAATATATATGTCGATTTGATAAA 1977

QY 271 sLysTyr----- 273
    |||||: |||||:
    1978 CAAATGCAATTAAGAGTTTCTGATTCAGATATGATGATTTATATTCGCTTT 2037

QY 274 -----TyrMetLysLeuLysAsnPhe----- 280
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    2038 ACTTTTGAGATGAAACCAAGAAATTTTAAATGAATTAATCTAATCTGCGAGAAAT 2097

QY 281 ----- 281
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    2098 AACTTAATTAATTAATGATTAATTAAGAAAGTTCAGCAATTTCCGTTGATTAATCG 2157

QY 281 tValAsnArgValPhe-----IleProThrLys 291
    |||||: |||||: |||||: |||||:
    2158 AGTAAATCGATATTTTCTTTTTCGAAAAATATTAATCTCACTCAATTAATTCACAGAC-AA 2216

QY 291 sPhePheAsnLysGluIleArgLys----- 299
    |||||: |||||: |||||: |||||:
    2217 GTGATTT---AAAGAAATTAAGCAATTTATATGATTTATGTCGATGAAGAAACATTTAGG 2273

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QY 300 -----ProSerLysAlaLeuLysGluLysVal 308
    |||||: |||||: |||||: |||||:
    2274 GAATTAAGGAGCTATTAATGATTTTCCAGTTATTAACAAATATACATTGAAAAA--- 2331

QY 308 lSerThrAspThrLysAspLeu----- 315
    |||||: |||||: |||||: |||||:
    2332 -AAAGTACATCTAATAATATATAGACAAATATCTTTTCGAAAAAACAATGTTACCAATTT 2390

QY 315 ----- 315
    |||||: |||||: |||||: |||||:
    2391 TAATCTTTGAAAAAATATTAAGATTTATCATTAAGATTCAGATTAATAACTT 2450

QY 316 -----PheGlu-----AsnLysIleGlyGlnGlyThrValAspPhePheAsn-- 329
    |||||: |||||: |||||: |||||:
    2451 TTTGACTTCTCTTGAATAATTAATGAATTTGATTTCAAGTTTATCATGCTTCAAAAT 2510

QY 330 -----LysGluIleArgAspProSerLysAlaLeuLysGluLysValSerAsnAspAl 347
    |||||: |||||: |||||: |||||:
    2511 TGTAAAAAATATTTTACTAATTAATTCAGAGGCTTAAGAAATTAAGACCACTATCG 2570

QY 347 aLysAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnAsnGlu 367
    |||||: |||||: |||||: |||||:
    2571 TAAATAATATTTTATCAAGATTAATATCAAAATATGTTGATATGCTGCTTGAAT 2630

QY 367 eArgAsp-----ProSerLysAlaLeuIleArgLysValSerThrGlyAlaGluAspLe 385
    |||||: |||||: |||||: |||||:
    2631 AGATGATTTATTAATTAATCAAGAAATTTACTTAATTTGATTTAATATGATGATTA 2690

QY 385 uPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnAsnGluIleArgAspPr 405
    |||||: |||||: |||||: |||||:
    2691 T-----TCTTAATTTTATAGGACGATTTTATACCTTAAGAAAT--- 2727

QY 405 oSerLysAlaLeuIleArgLysValTyrThrGlnAlaAspLeuPheGluAsn 423
    |||||: |||||: |||||: |||||:
    2728 -AGTTCATATTAATTTGAAAAATTTATTAATAAATATAGATCAATATATTAAT 2781

RESULT 20
US-08-910-551B-1
; Sequence 1, Application US/08910551B
; Patent No. 5910571
; GENERAL INFORMATION:
; APPLICANT: Sylvain Moineau, Barbara
; APPLICANT: J. Holler, Peter A. Vandenberg,
; APPLICANT: Edenezer R. Vedamuthu, Jeffrey K.
; APPLICANT: Kondo
; TITLE OF INVENTION: DNA Encoding Phage
; TITLE OF INVENTION: Abortive Infection Protein
; TITLE OF INVENTION: From Lactococcus
; TITLE OF INVENTION: Lactis, and Method of Use Thereof
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ian C. McLeod
; STREET: 2190 Commons Parkway
; CITY: Okemos
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48864
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 5.25 inch,
; MEDIUM TYPE: 360 kb storage
; COMPUTER: Acer
; OPERATING SYSTEM: MS-DOS (version 4)
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910, 551B
; FILING DATE: August 11, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/565, 907
; FILING DATE: December 1, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ian C. McLeod
; REGISTRATION NUMBER: 20,931

```

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REFERENCE/DOCKET NUMBER: Quest 4.1-158
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEFAX: (517) 347-4103
TELEX: No. 5910571e
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4467
TYPE: Nucleotide
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE:
DESCRIPTION: Genomic DNA
HYPOHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N/A
ORIGINAL SOURCE:
ORGANISM: Lactococcus lactis
STRAIN:
INDIVIDUAL ISOLATE: W1
DEVELOPMENTAL STAGE: N/A
HAPLOTYPE: N/A
TISSUE TYPE: N/A
CELL TYPE: bacterium
CELL LINE: N/A
ORGANELLE: N/A
IMMEDIATE SOURCE:
LIBRARY: genomic
CLONE: SMO-20
POSITION IN GENOME: N/A
FEATURE:
NAME/KEY: phage abortive infection
LOCATION: N/A
IDENTIFICATION METHOD: sequencing
OTHER INFORMATION: DNA encoding phage
PUBLICATION INFORMATION: resistance
PUBLICATION INFORMATION: N/A
US-08-910-551B-1

Alignment Scores:
Pred. No.: 0.11 Length: 4467
Score: 100.00 Matches: 96
Percent Similarity: 31.94% Conservative: 57
Best Local Similarity: 20.04% Mismatches: 121
Query Match: 4.24% Indels: 206
DB: 2 Gaps: 23

US-09-807-459-2 (1-458) x US-08-910-551B-1 (1-4467)
QY 129 GLLYSASNHISERTYRPE----- 135
DB 1411 GGAANAATCGAATCTTTTAAAGTATTTAATGGAATCCTTGCGAATATTTA 1470
QY 136 -----HisAspleuValPheAsnLeuLeuGluLys----- 145
DB 1471 AGSAGTCAGATTTTAAACACATTTTAACGCTAAAAACCTATACACAGACCAGTA 1530
QY 146 -----AsnValThrArgSpAlaAspAlaThrAspIleGluAsnPheAlaSerArgTyr 153
DB 1531 TATTTAAATTCACAAAATAATAGACGTAAGACAAATATAGATGCCCAATTTATAC 1590
QY 164 LeuTyrMetAlaThrLeuTyrTyr-----LysThrTyrThrAsnVal--- 177
DB 1591 AGTTAATAGCATTAATTAATATATATGTCACAAATAAAAAGATTTATGAAGATTTT 1650
QY 178 -----AspGluupheGlyAlaSer---PhePheAsnLysLeuSerPhe----- 190
DB 1651 ATTGATTAACAATTTTCAACGTCGCAAAATTTTATCAATGATTTGATTTCTCTAAG 1710
QY 191 -----ThrThrGlyLeuPheGlyTyrPglYlLeuLysArgAlaLeuLysGln 205
DB 1711 ACACAAAGAAATTAACACAAACATTAATATATGGA---GGAATAAAGAAA----- 1755

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QY 206 IleIleArgSerAsnLeuProLeuAspIleGlyThr-----GluHis 219
DB 1756 -----TTACATTTAGATTTATCTAAATTTTATCATCTTTATATACACT 1800
QY 220 SerVal-----SerArgLeuGlnHisIleThrSerSerTyr 231
DB 1801 AGTATACCATGATGATGATGTAAGAAATTCGATCTCAACAAATATGAAAAAGGGTTT 1860
QY 232 LysAspTyrMetLysPthrGlnIleProAlaLeuProLysPhe-AlaLysArgPheSerIle 251
DB 1861 TCTAATATACATTAATGATCTTTGATTAACGCTGT---CAATACACGCAACACATGCGATT 1917
QY 251 uMetValValGlnArgLeuValThrValAlaGlyTyrValLysPheProIrrPrrly 271
DB 1918 CCAACTGGAATATCTATGCTAGGATTAATACCGAACATATATATGCGCATTTGATAA 1977
QY 271 slYstrp----- 273
DB 1978 CAATGGAATATATGAAGATTGTGTATTCAGATATGATGATTTATATTCGGTTT 2037
QY 274 -----TyrMetLysLeuLysAsnPhe----- 280
DB 2038 ACTTTGAGAAATGAAAAAGCAAAATTTTAAATGAATTAATCTAATCTGTCGAGAAAT 2097
QY 281 ----- 281
DB 2098 AACTTAATTTATATGATTAATAAAGCAAGTGACAAATTCGCCGTTTGTGATTAATCG 2157
QY 281 LValAsnArgValPhe-----IleProThrLysIly 291
DB 2158 AGTAAATCGCATATTTTCTTTTGTGAATATTTACTTCAACTAATTCACAGC- AA 2216
QY 291 sPhePheAsnLysGluIleArgGlu----- 299
DB 2217 GTGGATT---AAAGAAATATAGCAATTTATATGATTTGTGTAATGACAAACATTTAGC 2273
QY 300 -----ProSerLysAlaLeuLysGluLysVal 308
DB 2274 GATTAAGGAGCTATTAATATGATTTTCCAGTATTAACAAATACATTTGAACAAAA--- 2331
QY 308 lSerThrAspThrLysAspleu----- 315
DB 2332 -AAAGTAGATACATAAAATATAGACAAATATCTTTGCAAAAGAACATGGTACCAATTT 2390
QY 315 ----- 315
DB 2391 TAATGTTTTGCAAAAAATATATGATTTATCATTAATAAAGATTCAAGATTAACTAATAGTT 2450
QY 316 -----PheGlu-----AsnLysIleGlyGlnGlyThrValAspPheAsn-- 329
DB 2451 TTTGACTTTTCTTGAAATATATTAATGATTTGGAATTTTCAAGTTTACAGCTTCAATAT 2510
QY 330 -----LysGluIleArgAspProSerLysAlaLeuLysGluLysValSerAsnSpAl 347
DB 2511 TGTAAAAAATATTTAGTAATATTAATTCAAAGGGCTTAAAGAAAAAATAACACACTATCG 2570
QY 347 aLysAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnAsnGluI 367
DB 2571 TAAAAATTAATTTATATCAACAAATATATCAAAATATGTTGTATATGTTCTCTTTGGA 2630
QY 367 earGasp-----ProSerLysAlaLeuIleArgLysValSerThcGlyLagLysPle 385
DB 2631 AGATGATTTATTAATTCACAAAGAAATTAATTAATGATTTAAATATTTGATGATTA 2690
QY 385 upheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnAsnGluIleArgAspR 405
DB 2691 T-----TCTTAATTTTGAAGAGATTTATACCTAAAGAT----- 2727
QY 405 oSerLysAlaLeuIleArgLysValIyrThrGluAlaAspAspleuPheGluAsn 423
DB 2728 -AGTTCATATTAATTAATGAAAAATTAATTAATAAATAAGATCAATTAATTAATTAAT 2781

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RESULT 21

US-08-909-425A-1  
: Sequence 1, Application US/08909425A  
: Patent No. 5928688  
: GENERAL INFORMATION:  
: APPLICANT: Sylvain Molneau, Barbara  
: APPLICANT: J. Holler, Peter A. Vandenberg,  
: APPLICANT: Ebenezer R. Vedamuthu, Jeffrey K.  
: APPLICANT: Kondo  
: TITLE OF INVENTION: DNA Encoding Phage  
: TITLE OF INVENTION: Abortive Infection Protein  
: TITLE OF INVENTION: From Lactococcus  
: TITLE OF INVENTION: Lactis, and Method of Use Thereof  
: NUMBER OF SEQUENCES: 1  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Ian C. McLeod  
: STREET: 2190 Commons Parkway  
: CITY: Okemos  
: STATE: Michigan  
: COUNTRY: USA  
: ZIP: 48864  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Diskette 5.25 inch,  
: MEDIUM TYPE: 360 kb storage  
: COMPUTER: Acer  
: OPERATING SYSTEM: MS-DOS (version 4)  
: SOFTWARE: Wordperfect 5.1  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/909,425A  
: FILING DATE: August 11, 1997  
: CLASSIFICATION: 435  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: 08/565,907  
: FILING DATE: December 1, 1995  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Ian C. McLeod  
: REGISTRATION NUMBER: 20,931  
: REFERENCE/DOCKET NUMBER:  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (517) 347-4100  
: TELEFAX: (517) 347-4103  
: TELEX: No. 5928688e  
: INFORMATION FOR SEQ ID NO: 1:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 4467  
: TYPE: Nucleotide  
: STRANDEDNESS: Single  
: TOPOLOGY: Linear  
: MOLECULE TYPE:  
: DESCRIPTION: Genomic DNA  
: HYPOTHEICAL: NO  
: ANTI-SENSE: NO  
: FRAGMENT TYPE: N/A  
: ORIGINAL SOURCE:  
: ORGANISM: Lactococcus lactis  
: STRAIN:  
: INDIVIDUAL ISOLATE: W1  
: DEVELOPMENTAL STAGE: N/A  
: HAPLOTYPE: N/A  
: TISSUE TYPE: N/A  
: CELL TYPE: bacterium  
: CELL LINE: N/A  
: ORGANELLE: N/A  
: IMMEDIATE SOURCE:  
: LIBRARY: genomic  
: CLONE: SMQ-20  
: POSITION IN GENOME: N/A  
: FEATURE:  
: NAME/KEY: phage abortive infection  
: LOCATION: N/A  
: IDENTIFICATION METHOD: sequencing  
: OTHER INFORMATION: DNA encoding phage  
: OTHER INFORMATION: resistance  
: PUBLICATION INFORMATION: N/A

US-08-909-425A-1  
Alignment Scores:  
Pred. No.: 0.11 Length: 4467  
Score: 100.00 Matches: 96  
Percent Similarity: 31.94% Conservative: 57  
Best Local Similarity: 20.04% Mismatches: 121  
Query Match: 4.24% Indels: 206  
DB: 2 Gaps: 23  
US-09-807-459-2 (1-458) x US-08-909-425A-1 (1-4467)  
QY 129 GLYASASnHISerTYrPhe-----LysThrTYrThrAsnVal--- 135  
DB 1411 GGAATAATCAGATTCTTTTATTTTAAAGTATTATATGAAATCCTTTGACATTATTTA 1470  
QY 136 -----HisAspLeuValPheAsnLeuGluLys----- 145  
DB 1471 AGAGTCATGATTGTAACACATTGTAACGTTAAACCTCTATCAACAGACCCAGTA 1530  
QY 146 -----AsnValThrArgAspAlaAspAlaThrAspIleGluAsnPheAlaSerArgTYr 163  
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QY 164 LeuTYrMetAlaThrLeuTYrTYr-----LysThrTYrThrAsnVal--- 177  
DB 1591 AGTTATATGCGATTAAATATATATATATATGTCACATAAAAAAGAGTTATATGAAGTATTT 1650  
QY 178 -----AspGluPheGlyAlaSer---PhePheAsnLysLeuSerPhe----- 190  
DB 1651 ATGTATACAAATTTTCAACGCAAAATTTTAAATCAATGGAATTTGATTATTCCTAAG 1710  
QY 191 -----ThrGlyLeuPheGlyTPGlyIleLysArgAlaLeuLysGln 205  
DB 1711 ACACAGAATATACACAAACATATATATATGGA---GGAATTAACAA--- 1755  
QY 206 IleIleArgSerAsnLeuProLeuAspIleGlyThr-----GluHis 219  
DB 1756 -----TTCATTATGATTTATCTAATTTTATCATCTTATATATACAT 1800  
QY 220 SerVal-----SerArgLeuGlnHisIleThrSerSerTYr 231  
DB 1801 AGTATACCATGATGATTCATGAGAAATCTGCATCTTAACAAATAGAAAAAGGTTT 1860  
QY 232 LysAspTYrMetAspThrGlnIleProAlaLeuProLysPhe-AlaLysArgPheSer 251  
DB 1861 TCTATATACATTAAGATACCTTGATTCAGCTGT---CAATACGAGAAACATGCGATT 1917  
QY 251 uMeCValValGlnArgLeuAlaThrValAlaGlyTYrValAspThrProTPPTyTyL 271  
DB 1918 CCACCTGGAAATCTATGTCAGATTTATTCGCAACATATATGCTGCCATTGGATAA 1977  
QY 271 sLYsTRP----- 273  
DB 1978 CAATGGAAATATAGAACTTTGCTATTCAGATATGATGATTTATATTCGGTTT 2037  
QY 274 -----TYrMetLysLeuLysAsnPhe----- 280  
DB 2038 ACTTTTGAGATGAAACAGCAAGATTTTAAATGAATTAATCTAATCTGCGAGAAAT 2097  
QY 281 -----Me 281  
DB 2098 AACTTAATTAATTAATGATTAATAAAGAAAGTGCACAAATTCGGTTTGTGATTAATCG 2157  
QY 281 tValAsnArgValPhe-----IleProThrLysLys 291  
DB 2158 AGTAAATCGATATTTTCTTTTCTTTTGAATAATATTAATCAACTAATTTCCACAGAC-AA 2216  
QY 291 sPhePheAsnLysGluIleArgLys----- 299  
DB 2217 GTGCAAT---AAAGAAATTAACAAATTTATAGATTATGTCGATGAAGAATTTAGG 2273  
QY 300 -----ProSerLysAlaLeuLysGluLysVal 308

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Db 2274 GAATAGGAGCTATATAATGATTTTCCACTATATACCAATACATGTAACAAAAA-- 2331
QY 308 lSerThrAspThrLysAspLeu----- 315
Db 2332 -AAAGTACTACTATAAATATGACAAATCTTTTCGAAAAAGAACAGGTTACCAATT 2390
QY 315 ----- 315
Db 2391 TAATGTTTTCGAAAAAATATAGATTATTCATTAAAGATTCAGATTACATAAGTT 2450
QY 316 -----PheGlu-----AsnLysIleGlyGlnGlyThrValAspPheAsn-- 329
Db 2451 TTTGACTTCTTTGAAAAATATTAAGAAATTTGAGATTTCAGATTATCAGTTCAAAATAT 2510
QY 330 -----LysGluIleArgAspProSerLysAlaLeuLysGluLysValSerAsnAspAl 347
Db 2511 TGTAAAAAATTTTACTAGTAATTAATCAAGGCTTAAAAAGAAATAAGACCCTATCG 2570
QY 347 alysAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnAsnGluI 367
Db 2571 TAAAAATATTTTATCAAGATTTATATCAATATTTGTTATATGCTTCTTGAAT 2630
QY 367 eaArgAsp-----ProSerLysAlaLeuIleArgLysValSerThrGlyAlaGluAsp 385
Db 2631 AGATGATTTTAAATCAAGAAAGAAATTAATACTTAATGATTAAATATGATGATTA 2690
QY 385 uPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnAsnGluIleArgAsp 405
Db 2691 T-----TCCTTAATTTAGGAGCAATTTTATACCTAAAGAAAT----- 2727
QY 405 oSerLysAlaLeuIleArgLysValLysThrGluAlaAspAspLeuPheGluAsn 423
Db 2728 -AGTTCATRTAATATGAAAAATTTATAAAAAAATAGATCAATTTATTATTAAAT 2781

RESULT 22
US-08-229-781-27
; Sequence 27, Application us/08229781
; Patent No. 5589174
; GENERAL INFORMATION:
; APPLICANT: Yoshinobu OKUNO et al.
; TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/229,781
; FILING DATE: April 19, 1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/054,016
; FILING DATE: April 29, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 27 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1754 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to genomic RNA
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: A/Sults/1/89
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:

US-08-229-781-27

Alignment Scores:
Pred. No.: 0.0269 Length: 1754
Score: 99.50 Matches: 58
Percent Similarity: 35.32% Conservative: 37
Best Local Similarity: 21.56% Mismatches: 89
Query Match: 4.22% Indels: 85
DB: 1 Gaps: 13

US-09-807-459-2 (1-458) x US-08-229-781-27 (1-1754)
QY 195 pheGlyTTPGlyIleLysArgAlaLeuLysGlnIleIleArgSerAsnLeuProLeuAsp 214
Db 852 TTTGGGTGAGA-----ATCATCCTCAACACCATCATGAT 890
QY 215 lleGlyThrGlnHisSerValSerArgLeuGlnHisIleThrSerSer-----TyrLys 232
Db 891 GAATGTGACGCGAAGTGTCAAAACACCCGAGGAGCTATTAACAGTAGTCTTCTTCAG 950
QY 233 AspTyrMetAspThrGlnIleProAlaLeuProLysPheAlaLysArgPheSerLeuMet 252
Db 951 AATGTACACCCAGTCAATAGAGAGTGTCCAAAGTATGTACAGGAGTACAAATTAAG 1010
QY 253 ValVal-----GlnArgLeuLeuAlaThrVal 261
Db 1011 ATGGTTACAGACTAAGAACATCCCATTCATTCACAGAGGTTGTGGAGCATT 1070
QY 262 AlaGlyTyrValAspThrProTTP-----TyrLysLysTTPtyr----- 274
Db 1071 GCCGTTTCATTGAAGGGGGGTGACTGTGAATGATAGATGTATGTTATCATCAT 1130

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QY 275 -----MelLyLeuLysasn 279
Db 1131 CAGATGACAAAGATGCTGCTATGCTGGGATCAAAAAACACACAAATGCCATTAC 1190
QY 280 PheMetValAsnArgVal-----PheIleProThr 289
Db 1191 GGAATTACAAACGAAGTCAATTCTGTATCGAAGAAATGAACACTCAATTTCACAGCTGTG 1250
QY 290 LysLysPhePheAsnLysGluIleArgGluProSerLysAlaLeuLysGluLysValSer 309
Db 1251 GGCAGGACTTTCAGTCAATTCATGATGATGATGATGATGATGATGATGATGATGATGAT 1307
QY 310 ThrAspThrLysAsp-----LeuPheGluAsnLys 319
Db 1308 GATGATTTCTGACATTTGGACATATATATGACAGATTTGTTGTTCTCTGCAAAAT--- 1364
QY 320 IleGlyGlnGlyThrValAspPheAsnLysGluIleArgAspProSerLysAlaLeu 339
Db 1365 -----GAAAGGACTTTCAGTCAATTCATGATGATGATGATGATGATGATGATGATGAT 1418
QY 340 LysGluLysValSerAsnAspAlaLysAspLeuPheGluAsnLysIleGlyGlnGlyThr 359
Db 1419 AAAAGCCATTAAAGATTAATGCCAAGAA-----ATAGGATACGGGTGT 1463
QY 360 ValAspPhe-----IleAsnAsnGluIleArgAspProSerLysAlaLeuIleArg 376
Db 1464 TTGGAATTCCTACCAAGTGTAAACATGAA-----TGCATGGAA 1502
QY 377 LysValSerThrGlyAlaGluAspLeu-----PheGluAsnLysIleGlyGln 392
Db 1503 AGTGTGAAAAATGGAAGTCTTATGACTATCCAAATATTTCCGAGAAATCAAGTTAAACAGG 1562
QY 393 GlyThrValAspPheIleAsnAsnGlu 401
Db 1563 GAAAAAATTGATGATGATGATGATGAA 1589

RESULT 23
US-08-630-918-27
; Sequence 27, Application US/08630918
; Patent No. 5631350
; GENERAL INFORMATION:
; APPLICANT: Yoshinobu OKUNO et al.
; TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,918
; FILING DATE: April 5, 1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/229,781
; FILING DATE: April 19, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/054,016
; FILING DATE: April 29, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:

```

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; TELEX:
; INFORMATION FOR SEQ ID NO: 27 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1754 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to genomic RNA
; ORIGINAL SOURCE:
; ORGANISM: A/SuItca/L/89
; US-08-630-918-27

Alignment Scores:
Pred. No.: 0.0269 Length: 1754
Score: 99.50 Matches: 58
Percent Similarity: 35.32% Conservative: 37
Best Local Similarity: 21.56% Mismatches: 89
Query Match: 4.22% Indels: 85
DB: 1 Gaps: 13

US-09-807-459-2 (1-458) x US-08-630-918-27 (1-1754)
QY 195 PheGlyThrProGlyIleLysArgAlaLeuLysGlnIleIleArgSerAsnLeuProLeuAsp 214
Db 852 TTGGGCTCAGGA-----ATCATCACCCTCAACGCAATCATGAT 890
QY 215 IleGlyThrGlnHisValSerValSerArgLeuGlnHisIleThrSerSer-----TyrLys 232
Db 891 GAATGTGACGGGAGGTGCAACACACCCAGGACCTAATAACAGTAGCTTCCTTCAG 950
QY 233 AspTyrMetAspThrGlnIleProAlaLeuProLysPheAlaLysArgPheSerLeuMet 252
Db 951 AATGTACACCCAGTCACATAGAGAGAGTGTCCAAAGTAGTCAGAGTACAAATTTAAGG 1010
QY 253 ValVal-----GlnArgLeuLeuAlaThrVal 261
Db 1011 ATGTTACAGAGCTAAGAACATCCATTCATTCACAGAGTTCTTTCGAGCCATT 1070
QY 262 AlaGlyTyrValAspThrProTrp-----TyrLysLysTyrPyr----- 274
Db 1071 GCCGGTTTCATTGAAGGGGGGTGACGTGAATGATGATGATGATGATGATGATGATGATGAT 1130
QY 275 -----MelLyLeuLysasn 279
Db 1131 CAGATGACAAAGATCTGCTATGCTGGGATCAAAAAACACACAAATGCCATTAC 1190
QY 280 PheMetValAsnArgVal-----PheIleProThr 289
Db 1191 GGAATTACAAACGAAGTCAATTCTGTATCGAAGAAATGAACACTCAATTTCACAGCTGTG 1250
QY 290 LysLysPhePheAsnLysGluIleArgGluProSerLysAlaLeuLysGluLysValSer 309
Db 1251 GGCAGGACTTTCAGTCAATTCATGATGATGATGATGATGATGATGATGATGATGATGAT 1307
QY 310 ThrAspThrLysAsp-----LeuPheGluAsnLys 319
Db 1308 GATGATTTCTGACATTTGGACATATATATGACAGATTTGTTGTTCTCTGCAAAAT--- 1364
QY 320 IleGlyGlnGlyThrValAspPheAsnLysGluIleArgAspProSerLysAlaLeu 339
Db 1365 -----GAAAGGACTTTCAGTCAATTCATGATGATGATGATGATGATGATGATGATGAT 1418
QY 340 LysGluLysValSerAsnAspAlaLysAspLeuPheGluAsnLysIleGlyGlnGlyThr 359
Db 1419 AAAAGCCATTAAAGATTAATGCCAAGAA-----ATAGGATACGGGTGT 1463
QY 360 ValAspPhe-----IleAsnAsnGluIleArgAspProSerLysAlaLeuIleArg 376
Db 1464 TTGGAATTCCTACCAAGTGTAAACATGAA-----TGCATGGAA 1502
QY 377 LysValSerThrGlyAlaGluAspLeu-----PheGluAsnLysIleGlyGln 392
Db 1503 AGTGTGAAAAATGGAAGTCTTATGACTATCCAAATATTTCCGAGAAATCAAGTTAAACAGG 1562

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1      Oy      393  GlyTValaspPheIleasnAsnGlu 401
2      Db      1563  GAAAAAATTGATGCAGTGAATTGGAA 1589
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4      RESULT 24
5      US-09-004-422-27
6      : Sequence 27, Application US/09004422
7      : Patent No. 6337070
8      : GENERAL INFORMATION:
9      : APPLICANT: Yoshinobu OKUNO et al.
10     : TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
11     : TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
12     : NUMBER OF SEQUENCES: 58
13     : CORRESPONDENCE ADDRESS:
14     : ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
15     : STREET: 2033 K Street, N.W., #800
16     : CITY: Washington
17     : STATE: D.C.
18     : COUNTRY: U.S.A.
19     : ZIP: 20006
20     : COMPUTER READABLE FORM:
21     : MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
22     : COMPUTER: IBM Compatible
23     : OPERATING SYSTEM: MS-DOS
24     : SOFTWARE: Wordperfect 5.1
25     : CURRENT APPLICATION DATA:
26     : APPLICATION NUMBER: US/09/004,422
27     : FILING DATE: January 8, 1998
28     : CLASSIFICATION: 530
29     : PRIOR APPLICATION DATA:
30     : APPLICATION NUMBER: 08/443,862
31     : FILING DATE: May 22, 1995
32     : PRIOR APPLICATION DATA:
33     : APPLICATION NUMBER: 08/229,781
34     : FILING DATE: April 19, 1994
35     : PRIOR APPLICATION DATA:
36     : APPLICATION NUMBER: 08/054,016
37     : FILING DATE: April 29, 1993
38     : ATTORNEY/AGENT INFORMATION:
39     : NAME: Warren M. Cheek, Jr.
40     : REGISTRATION NUMBER: 33,367
41     : REFERENCE/DOCKET NUMBER:
42     : TELECOMMUNICATION INFORMATION:
43     : TELEPHONE: 202-721-8200
44     : TELEFAX: 202-721-8250
45     : TELEX:
46     : INFORMATION FOR SEQ ID NO: 27 :
47     : SEQUENCE CHARACTERISTICS:
48     : LENGTH: 1754 base pairs
49     : TYPE: nucleic acid
50     : STRANDEDNESS: double
51     : TOPOLOGY: linear
52     : MOLECULE TYPE: cDNA to genomic RNA
53     : HYPOTHETICAL:
54     : ANTI-SENSE:
55     : FRAGMENT TYPE:
56     : ORIGINAL SOURCE:
57     : ORGANISM: A/suIta/1/89
58     : STRAIN:
59     : INDIVIDUAL ISOLATE:
60     : DEVELOPMENTAL STAGE:
61     : HAPOTYPE:
62     : TISSUE TYPE:
63     : CELL TYPE:
64     : CELL LINE:
65     : ORGANELLE:
66     : IMMEDIATE SOURCE:
67     : LIBRARY:
68     : CLONE:
69     : POSITION IN GENOME:
70     : CHROMOSOME/SEGMENT:
71     : MAP POSITION:

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UNITS:	FEATURE:
NAME/KEY:	LOCATION:
IDENTIFICATION METHOD:	OTHER INFORMATION:
PUBLICATION INFORMATION:	AUTHORS:
TITLE:	JOURNAL:
VOLUME:	ISSUE:
PAGES:	DATE:
DOCUMENT NUMBER:	FILING DATE:
PUBLICATION DATE:	RELEVANT RESIDUES IN SEQ ID NO:
US-09-004-422-27	
Alignment Scores:	
Pred. No.:	0.0269
Score:	99.50
Percent Similarity:	35.32%
Best Local Similarity:	21.56%
Query Match:	4.22%
DB:	4
	Gaps: 13
US-09-807-459-2 (1-458) x US-09-004-422-27 (1-1754)	
QY 195 PheGlyTrpGlyIleLysArgAlaLeuLysGlnIleIleArgSerAsnLeuProLeuAsp 214	
DB 852 TTTCGGTCAGGA-----ATCATCCTCAACACGATCATGATGAT 890	
QY 215 IleGlyThrGlnHisSerValSerArgLeuGlnHisIleThrSerSer-----TyrIlys 232	
DB 891 GAATGTACACGGAGTGTCAACACCCCGAGGAGCTATTAACAGATGCTCTTCTTCAG 950	
QY 233 AspTyrMetAspThrGlnIleProAlaLeuProLysPheAlaLysArgPheSerLeuMet 252	:::
DB 951 AATGTACACCGACGACACATATGAGAGTGTCCAAAGATATGCAGAGTCACAAATTAAG 1010	
QY 253 ValVal-----GlnArgLeuLeuAlaThrVal 261	
DB 1011 ATGCTTACAGGACTAAGAACATCCATCCATTCATCCACAGAGTTTGTGGACCAT 1070	
QY 262 AlaGlyTyrValAspThrProTrp-----TyrLysLysTyrTyr----- 274	:::
DB 1071 GCCCGTTTCATGAAAGGGGGGTGGACTGCAATGATGATGATGATGATGATGATGAT 1130	
QY 275 -----MetLysLeuLysAsn 279	
DB 1131 CAGATGACACAGAGATGTGCTGTGCTGCGGATCAAAAAACACACAAATAATCCATT 1190	
QY 280 PheMetValAsnArgVal-----PheIleProThr 289	
DB 1191 GGAATTCACAAACAGAGGTGAATTCGTAAATCGACAAATGACATCCATTCACAGCTGTG 1250	
QY 290 LysLysPhePheAsnLysGlnIleArgGluProSerLysAlaLeuLysGluLysValSer 309	:::
DB 1251 GGCACAAAGATTCACAAACA---TTAGAAAGAAGATGGATACCTTAAATTAATAAAGTTGAT 1307	
QY 310 ThrAspThrLysAsp-----LeuPheGluAsnLys 319	
DB 1308 GATGGATTTTCGACATTTGACATATATATGACGAATTTGTGTTCTACTGCAAAAT--- 1364	
QY 320 IleGlyGlnGlyThrValAspPhePheAsnLysGlnIleArgAspProSerLysAlaLeu 339	
DB 1365 -----GAAGAGCTTGGATTTTCATGACTCAAAATGTCAAGACATCTGTATGACGAATA 1418	
QY 340 LysGluLysValSerAsnAspAlaLysAspLeuPheGluAsnLysIleGlyGlnGlyThr 359	
DB 1419 AAAAGCCAAATTAAGATTAATGCCAAAGAA---ATAGGATACGGGTGT 1463	





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QY 203 LeuLysGlnIleIleArgSerAsnLeuProLeuAspIleGlyThrGluHisSerValSer 222
    ::::: ||| |||||::: ||| ||| :::
Db 706 ---AATGAAACAGAAAGTCTCACTACTCTAGAAAAACCGACTTCACATCTATTAGGT 762
QY 223 ArgLeuGlnHisIleThrSer-----SerTyrLysAspTyrMetAsp 236
    ::::: ||| ||| ||| ||||| ||| |||
Db 763 TATGTGGTCCCATTAATCTGAAGATTAAACAAACAAATTAAGGCTTAAGAT 822
QY 237 -ThrGlnIleProAlaLeuProLysPheAlaLysArgPheSerLeuMetValGlnArg 256
    |||||::: ||||| ||| |||
Db 823 GATGCAAGTTA-----TTGCTAAAGGCACTCG----- 850
QY 256 GluLeuAlaThrValAlaGlyTyrValAspThrProTyrLysLysTyrPyrMetCly 276
    :::::
Db 850 ----- 850
QY 276 sLeuLysAsnPheMetValAsnArgValPheIleProThrLysLysPheAsnLysGly 296
    ||||| ||| ||| ||| ||| |||
Db 851 ----AAAAACTTT-----ACGATTAAGGCTCCAAACATGAA 882
QY 296 uIleArgGluProSerLysAlaLeuLysGluLysValSerThrAspThrLysAspLeuPh 316
    ::::: |||||::: ||| ::::: ||| |||
Db 883 GATGGCATCTGTGTCACATCTTGAC-GATTAATAGCAATACATGCGACATACATTAAAT 941
QY 316 eGluAsnLysIleGlyGlnGlyThrValAspPheAsnLysGluIleArgAspProse 336
    ||| ||| ||| |||||::: ||| |||
Db 942 AGAGAAAGAAC-----AAAAAGATGGCAAGATATTCA 974
QY 336 rLysAlaLeuLysGluLysValSerAsnAspAlaLysAspLeuPheGluAsnLysIleGly 356
    ::::: ||||| ||| ||| ||| ||| |||
Db 975 ACTAACTATTGATGCTAAAGCTTCAAAAGACTATTATTAAACAACATGAAATGATTATGG 1034
QY 356 yGlnGlyThrValAspPheIleAsnGlnIleArgAspProSerLysAlaLeuIleArg 376
    ||| ||||| ||| ||| ||| ||| |||
Db 1035 CTCAGGACTGCT-----ATCCACCCCTCAACAGAGTGAATTATAGC 1076
QY 376 GlyValSerThrGlyAlaLeuAspLeuPheGluAsnLysIleGlyGlnGlyThrValAs 396
    ||||| ||| ||| |||||::: ||| |||
Db 1077 ACTTGACAGCACTTCAATATGATGCTATCCATTTATGTATGAGTGAAGTAAAGAGA 1136
QY 396 PheIleAsnAsnGluIleArgAspProSerLysAlaLeuIleArgPheValTyrThrGly 416
    ::::: ||| ||| ||| |||||::: ||| |||
Db 1137 ATAT---AATTAATTAAACCAAGTAAAGAAACCTCTCTCAACAGTTCCGATTAC 1193
QY 416 uAlaAspAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnLysGly 436
    ||||| ||||| ||||| |||||
Db 1194 AACTTCACAGTTCACTCAAAAAAATATTAAACGAATGATGGTTAATAACAAAC 1253
QY 436 uIleArgAsp 439
    ::::: |||
Db 1254 ATTAGACGAT 1263

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RESULT 28
US-08-688-988-9
; Sequence 9, Application US/08688988B
; Patent No. 609545
; GENERAL INFORMATION:
; APPLICANT: Lefebvre, Daniel D.
; APPLICANT: Malboobi, Mohammad A.
; TITLE OF INVENTION: PHOSPHATE STARVATION-INDUCIBLE PROTEINS
; FILE REFERENCE: PPL96-03
; CURRENT APPLICATION NUMBER: US/08/688,988B
; CURRENT FILING DATE: 1996-07-31
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 1829
; TYPE: DNA
; ORGANISM: Arabidopsis Thaliana
US-08-688-988-9
Alignment Scores:
Pred. No.: 0.0511 Length: 1829

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Score: 97.50 Matches: 77
Percent Similarity: 35.09% Conservative: 76
Best Local Similarity: 17.66% Mismatches: 132
Query Match: 4.13% Indels: 151
DB: 3 Gaps: 21
US-09-807-459-2 (1-458) x US-08-688-988-9 (1-1829)
QY 123 TrpMetArg---PheArgGlyLysAsnHis-----Ser 133
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Db 391 TGGCGAAGATTAATTTCTCTCATGGAGAAAGAGAAAGAGTGAAGTGAAGTGGTGGCA 450
QY 134 TyrPheHisAspLeuValPheAsnLeuGluLysAsnValThrArgAspAlaSerAla 153
    ::::: ||||| |||||::: ||| |||
Db 451 TTCTACCGACGCTCATCGAGCTCATTAATAATGGTTAACTCCA----- 498
QY 154 ThrAspIleGluAsnPheAlaSerArgTyrLeuTyrMetAlaThrLeuTyrTyrThr 173
    ::::: |||||::: ||| ||| |||
Db 499 -----TTGCTACTGTTTTCACGTGGACACT 525
QY 174 TyrThrAsnVal---AspGluPheGlyAla-----SerPhe 184
    ::::: |||||::: ||| ||| |||
Db 526 CCACAAAGATTTAAGAGATGAATATGGCGCTTTTAAGCGAAAGATTTGAGAGATTTC 585
QY 185 PheAsnLysLeuSerPheThrThrGlyLeuPheGlyTyrPyrLysArgAlaLeu--- 203
    ||| ||| ||| |||||::: ||| |||
Db 586 CGAGATATCGACATTTGTTTCCAAAGAAATACGCGAAAGATGAAACATTGGATCACT 645
QY 204 ---LysGlnIleIleArgSerAsnLeuProLeuAspIleGly----- 216
    ::::: ||||| ||| ||| ||| |||
Db 646 TTCAATAGCGCATGGGCTTTTCTGACGCTGCTATGACGTAGCGAAAGGACCTGCT 705
QY 217 ---ThrGluHisSerValSerArgLeuGlnHisIleThrSerTyrLysAspTyr 234
    ::::: ||| ||| |||||::: ||| |||
Db 706 CGTTCTCTCTTATACGTCATGCTAAATGCCAAGACGAGATCAGAGATGAGAGCTTAC 765
QY 235 MetAspThrGln----- 238
    ::::: |||
Db 766 CTGTGCACTCAAACTCTTATCTCTACGACGAAACAGTGAAGCTTACCGGAAATGC 825
QY 239 -----IleProAlaLeuProLysPheAlaLysArgPhe 249
    ::::: ||| ||| ||| |||
Db 826 GAAAGCTGAAGGTGGAGATCGGAAATTCACATATGCTCTGTCGGAAGCAGAT 885
QY 250 SerLeu-----MetValValGlnArgLeuAlaThrValAlaGly 263
    ||| ||| ||| |||||::: ||| |||
Db 886 GACCTTCTGATTCACAAAGACGCTGCTCATGACGCTGCACTTGACTTATTTGGGA 945
QY 264 ---TyrValAspThrProTyrTyrLysLysTyrTyrMetLysLeuAsnPheMetVal 282
    ::::: ||||| ||| ||| ||| |||
Db 946 TGGCATCTGACACAACTACATTTGGAGATTATCCACAGATCATGAAGACATTGGGA 1005
QY 283 AsnArgVal-----PheIleProThrLysLys----- 291
    ::|||::: ||| ||| ||| |||
Db 1006 CATAGATTGGCTAAATTTTACAACTGACGACAAAGCAAAAGCTTACCGATTTC 1065
QY 292 -----PhePheAsnLysGluIleArgGluProSerLysAla 303
    ::|||::: ||| ||| ||| ||| |||
Db 1066 GTTGGGCTCACTATATACCTAGTGTCTTCAACCATTTGAGAAACCTGATCTTCA 1125
QY 304 LeuLysGluLysValSerThrAspThrLysAspLeuGluAsnLysIleGlyGln--- 322
    ||| ||| ||| |||||::: ||| |||
Db 1126 ---AAACCAAGATGATGACAAAGATTCTTATTACATGGAGTCTAAGATGGCAAAAT 1182
QY 323 -----GlyThrValAspPhePheAsnLysGluIleArg 333
    ::|||::: ||| ||| ||| ||| |||
Db 1183 TAGCGCATTTGTAAGCAAGCTTTGACCGCTGCATTTGAACGCTTACGAGAGGTTTAGA 1242
QY 334 AspProSerLysAlaLeuLysGluLysValSerAsnAspAlaLysAspLeuPheGluAsn 353
    ||| ||| ||| |||||::: ||| |||
Db 1243 AGCTTTTGAAGTACATTAAAGACAAATACGCAAAATCCGAAATTTATGATCATGAGAAAC 1302
QY 354 LysIleGlyGln-----GlyThrValAsp----- 361

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Db 1303 GGATATGGAGAACTAGGGGCTCAGATCTGTTGCTGTGATCCCTGATCATAC 1362
      |||::: ||||| |||
Qy 362 -----PheIleasnsluileargaspProSerLyalaLeu---llearglys 377
      ::::: ::::: ::::: ||| |||
Db 1363 AGCAATATATTACTTCAGAGCATCTTTGAGTATGCAAGAAGCTGTTCATCGCAAA 1422
      ::::: ::::: :::::
Qy 378 ValSer---ThrGlyAla-----GluaspLeu 385
      |||::: |||||
Db 1423 GTGAATGTTCAGAGTACTTGTGTATGCTCATTTGTGATTAACCTCGAGTGAAGATGCT 1482
      |||::: |||||
Qy 386 PheIleasnsluileargaspProSerLyalaLeu---llearglys 405
      ::::: ::::: ||| ||||| |||||
Db 1483 TACAAACAGATTGGACTCTACAGCTGTTGATTTCAAAATTAACCTCACAGCT----- 1536
      |||::: |||||
Qy 406 SerLyalaLeuIleargLyValIleThrGluAlaAspPleuPheGluasnLysIle 425
      ::::: ::::: ||| |||
Db 1537 -----TACGAGAAAGAAATCC 1551
      |||::: |||||
Qy 426 GlyGlnGlyThrValAspPheIleasnLysGluIleargaspProSer 441
      |||::: |||||
Db 1552 GCGAAGTATTACAGAGATTCTCTCAGTCAAGGTTCGT---CCATCC 1596
      |||::: |||||
RESULT 29
PCT-US93-03077-2
: Sequence 2, Application PC/TUS9303077
: GENERAL INFORMATION:
: APPLICANT: Board of Regents, The University of Texas System
: APPLICANT: Gaynor, Richard B.
: APPLICANT: Wu, Foon Kin
: TITLE OF INVENTION: PROTEIN CELLULAR FACTOR USEFUL FOR
: TITLE OF INVENTION: REGULATING GENE EXPRESSION
: NUMBER OF SEQUENCES: 7
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold White & Durkee
: STREET: P. O. Box 4433
: CITY: Houston
: STATE: Texas
: COUNTRY: USA
: ZIP: 77210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent in Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/03077
: FILING DATE: 19930331
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/07/862,025
: FILING DATE: April 2, 1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Kammerer, Patricia A.
: REGISTRATION NUMBER: 29,775
: REFERENCE/DOCKET NUMBER: UFD270PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 713-787-1540
: TELEFAX: 713-749-2679
: TELEX:
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3279 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: unknown
: TOPOLOGY: unknown
: MOLECULE TYPE: cDNA
: PCT-US93-03077-2
Alignment Scores:
Pred. No.: 0.134 Length: 3279
Score: 97.50 Matches: 99
Percent Similarity: 33.67% Conservative: 66

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Best Local Similarity: 20.20% Mismatches: 196
Query Match: 4.13% Indels: 130
DB: 5 Gaps: 19
US-09-807-459-2 (1-458) x PCT-US93-03077-2 (1-3279)
Qy 9 AspValThrLysThrLeuLeuAlaIleSerGluSerVal-----AspSerAlaIle 25
      ::::: ||| |||||
Db 1135 GAAGTAATGAACATTACTTATACCCTGAGGAAGCAAGAAATGCAAGAGATGACGA 1194
      ::::: ||| |||||
Qy 26 AsnAlaTyrMetIleasnSerAspMetSerAspTyrLeu---SerAlaValSerAsp 44
      ::::: ||| |||||
Db 1195 AGTGAACCTCGTTAACTGTAACAGCAAGCTGATCTGTTCTCTACCAATAAAT 1254
      ::::: ||| |||||
Qy 45 PheAlaGluArgIleCysSerGlnValProLysGlySerAsnGlySerAlaSerVal 64
      ::::: ||| |||||
Db 1255 GAAGCAGACAGCTGTATAGCAAGGTG-----GCTGACAGCTGTAACCTGTGAAGT 1308
      ::::: ||| |||||
Qy 65 AlaTyrMetSerArgCysAlaLysGlnAsp---CysLeuThrLeuGlnSerLeuLysTyr 83
      ::::: ||| |||||
Db 1309 CAGCCGAAGACACTTCTGAGAAAGAGATGTTGCAAGACAGTGAATTTGTAATGAA 1368
      ::::: ||| |||||
Qy 84 ProLeuGluAlaLys---TyrGlnProLeuThrLeu---ProAspProTyrGlnLeuGln 101
      ::::: ||| |||||
Db 1369 AAGCTGAAAAAAGGAGGCTCAGTTATATCTCTTAGTAGAAGAAACACTTCTAGAA 1428
      ::::: ||| |||||
Qy 102 AlaAlaPheIleuPheLysGlu-----SerAspAlaAsnProAla 115
      ::::: ||| |||||
Db 1429 GAAGCTTTGATTAACCTGAAAGATGAATGTTGAGAGTGAAGAAAGCAAGTACACT 1488
      ::::: ||| |||||
Qy 116 AsnSerThrGluLysArgPheTyrPheTyrPheArgGlyLysAsnHisSerTyrPhe 135
      ::::: ||| |||||
Db 1489 TCTTCTTGAAAGATGATGTTACTCAAGAAATTCGAAAGCA----- 1530
      ::::: ||| |||||
Qy 136 HisAspLeuValPheAsnLeuGlnLysAsnVal-----ThrArgAsp 150
      ::::: ||| |||||
Db 1531 -----GAAAGAAAGTTCAACTACCTGCAAGAGAGAGAT 1566
      ::::: ||| |||||
Qy 151 AlaAspAlaThrAspIleGluAsnPheAlaSerArgTyrLeuTyrMetAlaThrLeuTyr 170
      ::::: ||| |||||
Db 1567 GCTGCTAAAAAGCAATCAAAAAATCAAAAAAGAA----- 1602
      ::::: ||| |||||
Qy 171 TyrLysThrTyrThrAsnValAspGluPheGlyAlaSerPheAsnLysLeuSerPhe 190
      ::::: ||| |||||
Db 1603 CTTCGCACATAGATTAAATAGTAGTAAGTGCAGACCTTTGAAAGAAAGATGACG 1662
      ::::: ||| |||||
Qy 191 ThrThrGlyLeuPheGlyTyrPheLysArgAlaLeuLysGlnIleIleArgSerAsn 210
      ::::: ||| |||||
Db 1663 ATCCGAGGTTAATGAGAGAGAGAAACCTTCAAAACAGCAGCTGCACATTTCTAAC 1722
      ::::: ||| |||||
Qy 211 Leu-----ProLeuAspIleGlyThrGluHisSerValSerArgLeuGln 225
      ::::: ||| |||||
Db 1723 ATCATCAAGAAATTAAGACCTAAAGCAAGCAAAATATGTTGCAAGAGCTGAAC 1782
      ::::: ||| |||||
Qy 226 HisIleThrSerSerTyrLysAspTyrMetAspThrGlnIleProAlaLeuProLysPhe 245
      ::::: ||| |||||
Db 1783 AAAAAAGTTAAAGAGCTTAGAGAGAGCTG----- 1812
      ::::: ||| |||||
Qy 246 AlaLysArgPheSerLeuMetValGlnArgLeuLeuAlaThrValAlaGlyTyrVal 265
      ::::: ||| |||||
Db 1813 -----CAGCATTTGAACAGCTCTTGATGCG----- 1839
      ::::: ||| |||||
Qy 266 AspThrProTyrTyrLysTyrPheLysLeuLysAsnPheMetValAsnArgVal 285
      ::::: ||| |||||
Db 1839 ----- 1839
      ::::: ||| |||||
Qy 286 PheIleProThrLysLysPheAsnLysGluIleArgGluProSerLysAlaLeuLys 305
      ::::: ||| |||||
Db 1840 -----AAGAGAGAGCTTGAGAAACACATAGAGAAATATTAAAAAACTAAAT 1887
      ::::: ||| |||||
Qy 306 GluLysValSerThrAspThrLysAspLeu----- 315
      ::::: ||| |||||
Db 1888 TCCATGCTGAACGCCAAGAAAGATCTTGCGCTTCAGGTAGACATGATGAACCTT 1947
      ::::: ||| |||||

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Db 3859 GAAAAAGTATTGAAGACGACATGATATATACGACGCGTTCGATGAGTGTAGAA 3915
|||||
RESULT 31
US-08-973-462-1
; Sequence 1, Application US/08973462B
; Patent No. 6191270
; GENERAL INFORMATION:
; APPLICANT: DRULHE, PIERRE
; APPLICANT: DAUBERES, PIERRE
; TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
; FILE REFERENCE: 0660-0125-0 PCT
; CURRENT APPLICATION NUMBER: US/08/973,462B
; CURRENT FILING DATE: 1998-02-06
; EARLIER APPLICATION NUMBER: PCT/FR96/00894
; EARLIER FILING DATE: 1996-06-12
; EARLIER APPLICATION NUMBER: FR 95/07007
; EARLIER FILING DATE: 1995-06-13
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6152
; TYPE: DNA
; ORGANISM: P. falciparum
US-08-973-462-1

Alignment Scores:
Pred. No.: 0.381 Length: 6152
Score: 97.50 Matches: 80
Percent Similarity: 39.10% Conservative: 76
Best Local Similarity: 20.05% Mismatches: 138
Query Match: 4.13% Indels: 105
Gaps: 20

US-09-807-459-2 (1-458) x US-08-973-462-1 (1-6152)
QY 109 GUGSERASPAALASNPALASNPASERHRCGLYSARGPHETRMETARGPHEARGARG 128
|||||
Db 3128 GAAAGTATGAAAGTGTTCGACAGATTTAGAGAA----- 3163
QY 129 GLYLSASNPASNPASNPASNPASNPASNPASNPASNPASNPASNPASNPASNPAS 146
|||||
Db 3164 -----TTAAGCAAGTGTATTAATGATGATTAAGTAACTAGAG 3205
QY 147 VALTHRARGASPAALASNPASNPASNPASNPASNPASNPASNPASNPASNPASNPAS 166
|||||
Db 3206 GAAACAGTAGAATTTAGCGGAGAAAGTTAGAAAC----- 3241
QY 167 ALATHRLEUITYTYTYTYTYTYTYTHRASNPASNPASNPASNPASNPASNPASNPAS 186
|||||
Db 3242 -----AATGAAATGATTAAGCATTTTGTAGT 3268
QY 187 LYSLEU-----SerPheThrGlyLeuPheGlyTyr 197
|||||
Db 3269 GAAATATTTGATTAATGTAAGAAAGATACAGAAATTTATTAAACGATATGTT----- 3322
QY 198 GLYILEUSARGALALEULYSGLINLEILEARGSERASNPASNPASNPASNPASNPASNP 217
|||||
Db 3323 -----CGAAGTATGAAACCGATATA-----GTAATCCAAATCA 3355
QY 218 GLUHSERVALSERARGLEUGLINHSILETHRSERSETYTYLYSASPTYRMEASPHR 237
|||||
Db 3356 GAAGAAAAGGTGATTTAAATGAAATGTCGTACTTCGATTTTATGATTAATATAGAAAT 3415
QY 238 GLINLEPROALALEUPROLYSPHEALALYSARGPHESETLEU----- 251
Db 3416 ATGAAAGAGGTTTATTAATAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3475
QY 252 METVALVALGINDARGLEULALEALATHRVALAAGLYTYRVALASPTHRPROTPYRYS 271
Db 3476 ACTGTAAGTCAATGTAAGCAAAATATATATGATGATGTTGATGATGATGATGATGATG 3535
QY 272 LYSTPTYRMEALYSLEULYSASNPHEMET-----VALASARGVALPHEILEPROTHR 289

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Db 3536 GATCATATTTTAGATATATTAATATGACGACGAGCGGTGAAAGAAATGTTTATATTG 3595
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QY 290 LYSLSYPHEPHEASNPGLU-----ILEARGLU---PROSERLYSALA 303
Db 3596 GAAAGTGTATTTAAAGCAAGTATGATTAATTAATTAATTAATTAATTAATTAATTAAT 3655
QY 304 LEULYSGLULYSVALSERTHRASPHRILYSASPLEUPHEGLUASNPILLEGLYINGLY 323
Db 3656 GTTCAAAAAGAGTACGAAAAAGAACTGTTACTATTATTGAA---GAAATGCAAGAAAT 3712
QY 324 THRVALASPPHEPHEASNPGLULLEARGSPROSER-----LYSALALEU 339
Db 3713 ATTGTAGATGTTTATGAGAGGAAAAAGATTTAACAAGACATGATGATGATGATGATGAT 3772
QY 340 LYSGLU-----LYSVALSERASNPASNPASNPASNPASNPASNPASNPASNPASNP 356
Db 3773 GAAAGATCCATGAAATATCTTCACATTTCTTAAGAAAGAAAGTATCTATTTAAAGAT 3832
QY 357 GLINGLYTHRVALASPPHEILEASNPASNPGLULLEARG-----ASPROSERLYS 372
Db 3833 GAAAAAGATGTTTCACTAGTGTTCGACAGAAAGTTCAACACATGATGATGATGATGAT 3892
QY 373 ALALEUILLEARGLYSVALSERTHRCGLYLAAGLUSAPLEUPHEGLUASNPILLEGLY 392
Db 3893 GAGAAAGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3946
QY 393 GLYTHRVALASPPHEILEASNPASNPGLULLEARGSPROSERLYSALALEULLEARG 412
Db 3947 -----GAAATTAATGACATTAAGCAAACTTATTGAGAA 3982
QY 413 VALTYR-----THRCGLUALASPP-----ASPLEUPHEGLUASNPILLEG 425
Db 3983 ACTCAAGTGAATGAATGACAGACAGATTTAATTAAGATGATGATGATGATGATGATG 4042
QY 426 GLYINGLYTHRVALASPPHEILEASNPGLULLEARGSPROSERLYSALALEULLE 445
Db 4043 TTAGAAAAAGCATTTATTCAGAGATTTCTAAGAAATTAATGATGATGATGATGATG 4102
QY 446 ARGLYSVAL-----SERTHRCGLUALASNPASNPGLULLE 457
Db 4103 GAAAAAGTATTGAAGACGACATGATATATACGACGCGTTCGATGAGTGTAGAA 4159

RESULT 32
US-08-799-138-5
; Sequence 5, Application US/08799138
; Patent No. 5994053
; GENERAL INFORMATION:
; APPLICANT: Verma, Desh Pal
; TITLE OF INVENTION: PHRAGMOPLASTIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CALFEE, HALTER & GRISWOLD
; STREET: 800 SUPERIOR AVENUE
; CITY: CLEVELAND
; STATE: OHIO
; COUNTRY: USA
; ZIP: 44114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/799,138
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLTRICK, MARY E
; REGISTRATION NUMBER: 34,829
; REFERENCE/DOCKET NUMBER: 22727/00139
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (216) 622-8458

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TELEFAX: (216) 241-0816
:
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2211 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 175..2004
: US-08-799-138-5

Alignment Scores:
Pred. No.: 0.0807 Length: 2211
Score: 97.00 Matches: 63
Percent Similarity: 35.908 Conservative: 63
Best Local Similarity: 17.958 Mismatches: 125
Query Match: 4.118 Indels: 100
DB: Gaps: 16

US-09-807-459-2 (1-458) x US-08-799-138-5 (1-2211)

QY 139 ValPheasnleuenuGluysasnValThrArgAspAlaLaspAlaThrAspIleGluAsn 158
DB 892 GTTGTAATAGATCACAACAAGACATMAACAAGAAATGTTGCTGCTAGGCGT 951
QY 159 PheAlaSerArgTyrLeuTyrMetAlaThrLeuTyrTyrLysThrTyrTrpAsnValAsp 178
DB 952 AGGAAGAGTGTAGTAC---TTTATAGTACCCCGAATATATAACACCTTGCAAC----- 1002
QY 179 GluPheGlyAlaSerPhePheasnLysLeuSerPheThrThrGlyLeuPheGlyTyrGly 198
DB 1003 AGAATGGGTTCTGACATCTGGCGAAGATG----- 1032
QY 199 IleLysArgAlaLeuLysGlnIleIleArgSerAsnLeuProLeuAspIleGlyThrGlu 218
DB 1033 CTCTCAAGCATTTGGAGACAGTAACTACCAAAATTCCT-----GGCATTCAA 1083
QY 219 HisSerValSerArg----- 223
DB 1084 TCCTTATTTAAACAACAATTCGCCGAACCTGAAGCTGAACCTACTGCTTAGGAAACCT 1143
QY 224 -----LeuGlnHisIleThrSer----- 230
DB 1144 GTTGACAGCTGATCTGGGCGAAGTGTATGCTATCATGGAATATGCCCTCATTTGAT 1203
QY 231 -----TyrLysAspTyrMet----- 235
DB 1204 CAAATATTAAAGACCATCTTGATGGCGTGGCGCTGGAGGTGATTAATTTATATGTC 1263
QY 236 ---AspThrGlnIleProAlaLeuProLys-----PheAlaLysArgPheSerLeu 251
DB 1264 TTGGACAAATAGCTCCCTGCTGCTTTAAANAAGTTGCAGTTGTATGAAGCAGCTTTCATG 1323
QY 252 MetValValGlnArgLeuLeuAlaThrValAlaGlyTyr-----ValAspThrPro 268
DB 1324 GAAATAATAGGAACCTTATTACAGAACTGATGGGTATGACGCCTCATTAATAGCTCA 1383
QY 269 TrpTyrLysLysTrpTyrMetLysLeuLysAsnPheMetValAsnArgValPheIlePro 288
DB 1384 -----GAACTAAGATACCGCTGCTGCTTAATGAATCTTCTAATTAACATTAAGGGCCCT 1437
QY 289 ThrLysLysPhePheasnLysGluIleArgGluProSerLysAlaLeuLysGluLysVal 308
DB 1438 GCTGAGTCAGCTGTGAT---GGCGTTCACTCCCTGTTAAAGACCTTGCTTCACAAAGCT 1494
QY 309 SerThrAspThrLysAspLeu-----PheGluAsnLysIleGlyGlnGly 323
DB 1495 ATGAGTGAGACTTTGGCTTGAAGCAGTATCTGTCTCCGGGTGAGGTTGGGGCTGCA 1554
QY 324 ThrValAlaPhePheasnLysGluIleArgAspProSerLysAlaLeuLysGluLysVal 343
DB 324 ThValAlaPhePheasnLysGluIleArgAspProSerLysAlaLeuLysGluLysVal 343

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DB 1555 TCTGTGATTACTCGAAGA---ATGAGGATGAAGAA--- 1593
QY 344 SerAsnAspAlaLysAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIle 363
DB 1594 ---AGAGCAACACTGCAGCTAGTATGATGAGTGGCATGCTGATGATTTCTTT 1650
QY 364 AsnAsnGluIleArgAspProSerLysAla-----LeuIleArgLysValSerThrGly 381
DB 1651 CGAAGCTTCTCAACATGTTGATTAAGGGTGGCAATCCACACATTCATTCATGATAGA 1710
QY 382 AlaGluAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnAsn--- 400
DB 1711 TATATGATTCAATCTCAAGCCAAATTGGAAACCACAAATTTGTCATATGATATAGTC 1770
QY 401 -----GluIleArgAspPro 405
DB 1771 TGTGCTACTGTGGGCAATTCATCCCAAGTCATGCTATTTGTCAGAGCGGAGGCA 1830
QY 406 SerLysAlaLeuIleArgLysValTyrThrGlu 416
DB 1831 AAAGCAAGTCACTGATCATCTTTTACCGAG 1863

RESULT 33
US-09-392-362-5
: Sequence 5, Application US/09392362
: Patent No. 6248868
: GENERAL INFORMATION:
: APPLICANT: Verma, Desh Pal
: TITLE OF INVENTION: PHRAGMOPLASTIN
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: CALFEE, HALTER & GRISWOLD
: STREET: 800 SUPERIOR AVENUE
: CITY: CLEVELAND
: STATE: OHIO
: COUNTRY: USA
: ZIP: 44114
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/392,362
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/799,138
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: GOLRIK, MARY E
: REGISTRATION NUMBER: 34,829
: REFERENCE/DOCKET NUMBER: 22727/00139
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (216) 622-8458
: TELEFAX: (216) 241-0816
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2211 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 175..2004
: US-09-392-362-5

Alignment Scores:
Pred. No.: 0.0807 Length: 2211
Score: 97.00 Matches: 63
Percent Similarity: 35.908 Conservative: 63
Best Local Similarity: 17.958 Mismatches: 125

```







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1 COUNTRY : USA
2 ZIP : 19406-2799
3
4 COMPUTER READABLE FORM:
5
6 MEDIUM TYPE: Floppy disk
7
8 COMPUTER : IBM PC compatible
9
10 OPERATING SYSTEM: PC-DOS/MS-DOS
11
12 SOFTWARE : Patent in Release #1.0, Version #1.25
13
14 CURRENT APPLICATION DATA:
15
16 APPLICATION NUMBER: PCT/US94/01149
17
18 FILING DATE:
19
20 CLASSIFICATION:
21
22 PRIOR APPLICATION DATA:
23
24 APPLICATION NUMBER: US 149,150
25
26 FILING DATE: 05-NOV-1993
27
28 PRIOR APPLICATION DATA:
29
30 APPLICATION NUMBER: US 013,415
31
32 FILING DATE: 01-FEB-1993
33
34 PRIOR APPLICATION DATA:
35
36 APPLICATION NUMBER: US 108,914
37
38 FILING DATE: 18-AUG-1993
39
40 PRIOR APPLICATION DATA:
41
42 APPLICATION NUMBER: US 837,773
43
44 FILING DATE: 18-FEB-1992
45
46 PRIOR APPLICATION DATA:
47
48 APPLICATION NUMBER: US 751,896
49
50 FILING DATE: 30-AUG-1991
51
52 PRIOR APPLICATION DATA:
53
54 APPLICATION NUMBER: US 387,200
55
56 FILING DATE: 28-JUL-1989
57
58 PRIOR APPLICATION DATA:
59
60 APPLICATION NUMBER: US 238,801
61
62 FILING DATE: 02-NOV-1988
63
64 PRIOR APPLICATION DATA:
65
66 APPLICATION NUMBER: US 645,732
67
68 FILING DATE: 30-AUG-1984
69
70 ATTORNEY/AGENT INFORMATION:
71
72 NAME: Baumeister, Kirk
73
74 REGISTRATION NUMBER: 33,833
75
76 REFERENCE/DOCKET NUMBER: P50134 PCT
77
78 TELECOMMUNICATION INFORMATION:
79
80 TELEPHONE: 215-270-5096
81
82 TELEFAX: 215-270-5090
83
84 INFORMATION FOR SEQ ID NO: 31:
85
86 SEQUENCE CHARACTERISTICS:
87
88 LENGTH: 912 base pairs
89
90 TYPE: nucleic acid
91
92 STRANDEDNESS: double
93
94 TOPOLOGY: unknown
95
96 MOLECULE TYPE: DNA (genomic)
97
98 FEATURE:
99
100 NAME/KEY: CDS
101
102 LOCATION: 1..912
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104 PCT-US94-01149-31
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[illegible]



OY 433 IleasnlysgluileargAspproserlysalaleuilearglyValSerThrgluAla 452  
DB 1471 TTAATATAGAAAAAGTAGATCAAGTGAACGGAGTAGATGAACGTTAAGTCTAATGAT 1530  
OY 453 Aspasnleu 455  
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RESULT 37  
US-08-471-044-31  
Sequence 31, Application US/08471044  
Patent No. 5840868  
GENERAL INFORMATION:  
APPLICANT: Warren, Gregory W  
APPLICANT: Kozziel, Michael G  
APPLICANT: Mullins, Martha A  
APPLICANT: Nye, Gordon J  
APPLICANT: Carr, Brian  
APPLICANT: Desai, Nalin M  
APPLICANT: Kostichka, N. Kristy  
APPLICANT: Duck, Nicholas B  
APPLICANT: Estruch, Juan J  
TITLE OF INVENTION: No. 5840868el Pesticidal Proteins and Strains  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: NY  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,044  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/463,483  
FILING DATE: 05-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/314,594  
FILING DATE: 09-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/218,018  
FILING DATE: 23-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/037,057  
FILING DATE: 25-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Pace, Gary M.  
REGISTRATION NUMBER: 40,403  
REFERENCE/DOCKET NUMBER: CGC 1695/CIP3/DIV6 - SOLV3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8582  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2612 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 118..2484  
OTHER INFORMATION: /note= "Native DNA sequence  
OTHER INFORMATION: encoding VIP3A(b) from AB424"

US-08-471-044-31  
Alignment Scores:  
Pred. No.: 0.123 Length: 2612  
Score: 96.50 Matches: 102  
Percent Similarity: 36.18% Conservative: 80  
Best Local Similarity: 20.28% Mismatches: 202  
Query Match: 4.09% Indels: 119  
DB: 2 Gaps: 24  
US-09-807-459-2 (1-458) x US-08-471-044-31 (1-2612)  
OY 4 SeraspserValgllyAspValThrlysrThrleuAlaIleaserGluSerValaspsr 23  
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DB 268 ATTTAAAGAAATCAGACACTAATAATGATATTCTCGTAAATTGAGGGGTGAATGCA 327  
OY 44 AsnPhaIaGluaTygIleCysSerGlnValProlysgIySerAsnCysSerAlaSerVal 63  
DB 328 AGCTTAAATGATCTTATCGACAG-----GGAACTTAAATACAGAAATTA 372  
OY 64 SerIaTyMetSerAspTygAlaIySgIAspCysleuThrleuGlnSerleuIysTy 83  
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DB 493 AGTGATGTAATCAAAATAATATGCGCTAAGTCGCAAAATAGAAATTAAGTAACAA 552  
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DB 553 TTGCAGAGATTTCTGANAAGTGGATTTATTAATGTAATGACTTAACTTCA 612  
OY 119 GluIysArgPheTrpMetArgPheArgArgIyLysAsn--HisSerTYrPheHisAsp 137  
DB 613 CTACTGAAATTTACACCGCGATCAAGATTAATATGTAAGCAAAATTTGAGCA 672  
OY 138 LeuValPhe--AsnleuLeuGluLysAsnValThrArgAspAlaAspAlaThrAspIle 156  
DB 673 TTAACCTTTGCTACAGAACTAGTTCAAAAGTAAGAAAGATGGCTCTCCAGATATT 732  
OY 157 GluAsnPhaIaSerArgTYrleuTYrMetAlaThrleuTYrTYrIysThrThrasn 176  
DB 733 CGTGATGAGTTAACTGACTTAACCTGACGAAAGTGAACAAATAATGATGTGAT 792  
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DB 793 GGTTCGATTTTACCTTAATATCATTCACGATGTAATGTAAGAAATAATTTATTCGG 852  
OY 197 ---TrpGlyIleLysArgAlaLeuLysGlnIleIleArgSerAsnleuProleu----- 213  
DB 853 CGTTCAGCTTTAAAACTGATCGGAATTAATTAATAAGAAAGATGTAAGAAAGAGTGC 912  
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DB 913 AGTAGGTCGGAATGTTTAACTCTCTAATTGATTAAACGCTGTGCA----- 963  
OY 229 SerSerTYrLysAspTYrMetAspThrGlnIleProAlaLeuProlyPheAlaLysArg 248  
DB 964 -----GCAAAACT 972  
OY 249 PheSerLeuMetValValGlnArgLeuLeuAlaThrValAlaGlyTYrValAspThrPro 268  
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Db 1303 ATTTATGAATGAACACTTTAAATATAGAAAAAGGAATTTAGAGTAAAC-----ATCCTC 1086
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Qy 288 ProThrlYsLysPhePheasnLYsGLuIlEaRgGLuProSerLYsAlaLeuLYsGLuLYs 307
      ||||| :::: ||| ||| ||| |||
Db 1087 CCTGACA-----CTTCTTAATTAACCTTTTCTTAATCCCAATTAATGCAAAAGTTAAAGGA 1137
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Qy 308 ValSerThrAspThrLYsAspLeuPheGLuAsnLYsIlEGlyGlnGLYThrValAspPhe 327
      ||| ||| ||| ||| ||| |||
Db 1138 AGTATGATGAAGATGCMAAGATGATGTGGGAAGCTAAACCGACATGCATGTATGGGT 1197
      ||| ||| ||| ||| ||| |||
Qy 328 PheAsnLYsGLuIlEaRgAspProSerLYsAlaLeuLYsGLuLYsValSerAsnAspAla 347
Db 1198 -----GAAATTAGTAATGATTCACA 1215
      :::: ||||| |||
Qy 348 -----LYsAspLeuPheGLuAsnLYsIlEGlyGlnGLYThrValAspPheIleAsn 364
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Qy 365 AsnGLuIlEaRgAspProSerLYsAlaLeuIlEaRgLYsValSerThGLYAlaGLuAsp 384
      :::: ||| :::: ||| ||| |||
Db 1258 TATCAAGATC-----GATTAAGATGCTCTATGCAAGATTATTAATGCGGATATGAT 1308
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Qy 385 -----LeuPheGLuAsnLYsIlEGlyGlnGLYThrValAspPheIleAsnAsnGLuIle 402
      ||| :::: ||| ||| ||| |||
Db 1309 AAATATTATGCGCCACGATCAATCTGGACAA-----ATCTATTATTAACAAATTAACATA 1359
      ||| :::: ||| ||| ||| |||
Qy 403 ArgAspProSerLYsAlaLeuIlEaRgLYsVal----- 413
      ||| ||| ||| ||| |||
Db 1360 GTATTTCCAATGAATATGTAAATTACTAAATTAATGATTCACATAAAATGAAACCTTA 1419
      :::: ||| ||| ||| |||
Qy 414 ---TYThrGLuAlaAspAspLeuPheGLuAsnLYsIlEGlyGlnGLYThrValAspPhe 432
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Db 1420 AGAATATGAGTAACACGCAATTTTATGTATCTTCACAGGAGAA-----ATTGAC--- 1470
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Db 1531 GATGGGGTG 1539

RESULT 38
US-08-463-483A-31
: Sequence 31 Application US/08463483A
: Patent No. 5845870
: GENERAL INFORMATION:
: APPLICANT: Warren, Gregory W
: APPLICANT: Koziele, Michael G
: APPLICANT: Mullins, Martha A
: APPLICANT: Nye, Gordon J
: APPLICANT: Carr, Brian
: APPLICANT: Deasli, Nalini M
: APPLICANT: Kostichka, N. Kristy
: APPLICANT: Duck, Nicholas B
: APPLICANT: Estruch, Juan J
: TITLE OF INVENTION: No. 5849870el pesticidal Proteins and Strains
: NUMBER OF SEQUENCES: 50
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: CIBA-GEIGY Corporation
: STREET: 7 Skyline Drive
: CITY: Hawthorne
: STATE: NY
: COUNTRY: USA
: ZIP: 10532
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30B
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/463,483A
:

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1      FILING DATE:
2      CLASSIFICATION: 530
3      PRIOR APPLICATION DATA:
4      APPLICATION NUMBER: US 08/314,594
5      FILING DATE: 09-SEP-1994
6      PRIOR APPLICATION DATA:
7      APPLICATION NUMBER: US 08/218,018
8      FILING DATE: 23-MAR-1994
9      PRIOR APPLICATION DATA:
10     APPLICATION NUMBER: US 08/037,057
11     FILING DATE: 25-MAR-1993
12     ATTORNEY/AGENT INFORMATION:
13     NAME: SFULL, W. Murray
14     REGISTRATION NUMBER: 32,943
15     REFERENCE/DOCKET NUMBER: CGC 1695/CIP3
16     TELECOMMUNICATION INFORMATION:
17     TELEPHONE: 919-541-8615
18     TELEFAX: 919-541-8689
19     INFORMATION FOR SEQ ID NO: 31:
20     SEQUENCE CHARACTERISTICS:
21     LENGTH: 2612 base pairs
22     TYPE: nucleic acid
23     STRANDEDNESS: single
24     TOPOLOGY: linear
25     MOLECULE TYPE: DNA (genomic)
26     HYPOTHETICAL: NO
27     FEATURE:
28     NAME/KEY: CDS
29     LOCATION: 118..2484
30     OTHER INFORMATION: /note="Native DNA sequence
31     OTHER INFORMATION: encoding VIP3a(b) from AB424"
32     US-08-463-482A-31

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Pred. No.:	0 123	Length:	2612
Score:	96.50	Matches:	102
Percent Similarity:	36.18%	Conservative:	80
Best Local Similarity:	20.28%	Mismatches:	202
Query Match:	4.09%	Indels:	119
DB:	2	Gaps:	24

  

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Db 235 ACGGTACAGAGTGGTGCATCTAAC-----CTGACAGCAA 267	235	ACGGTACAGAGTGGTGCATCTAAC-----CTGACAGCAA 267
QY 24 AlaIaAsnAlaIaIyrMetIleAsnSerAspMetSerAspIyrLeuSerAlaValSerAsp 43	24	AlaIaAsnAlaIaIyrMetIleAsnSerAspMetSerAspIyrLeuSerAlaValSerAsp 43
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QY 44 AsnPhenAlaGluATrGlyIleCysSerGlnValProLysGluSerAsnCysSerAlaSerVal 63	44	AsnPhenAlaGluATrGlyIleCysSerGlnValProLysGluSerAsnCysSerAlaSerVal 63
Db 328 AGCTTAATATGATCTTATTCGCACAG-----GGAACCTTAATATACGAAATTA 372	328	AGCTTAATATGATCTTATTCGCACAG-----GGAACCTTAATATACGAAATTA 372
QY 64 SerAlaIyrMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSerLeuLysTyr 83	64	SerAlaIyrMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSerLeuLysTyr 83
Db 373 TCTAAGCAAAATATTAAATTAATTCGAAATGACAAATACAACTTTAAATGATGTTAAATAC 432	373	TCTAAGCAAAATATTAAATTAATTCGAAATGACAAATACAACTTTAAATGATGTTAAATAC 432
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QY 92 -----LeuThrLeuProAspProTyr-----Gln 99	92	-----LeuThrLeuProAspProTyr-----Gln 99
Db 493 AGTATGTAAATGAAACAACAAATTAATCGCTAGTTCGCAATAGATATCTTAAGTAACAA 553	493	AGTATGTAAATGAAACAACAAATTAATCGCTAGTTCGCAATAGATATCTTAAGTAACAA 553
QY 100 LeuGluAlaAlaPheIleLeuPheLysGluSerAspAlaAsnPro---AlaAsnSerThr 118	100	LeuGluAlaAlaPheIleLeuPheLysGluSerAspAlaAsnPro---AlaAsnSerThr 118
Db 553 TTGCAAGAGATTTCTGCATTAAGTTCGATATTTATGTAATGAATGACTATTAACTTACACA 612	553	TTGCAAGAGATTTCTGCATTAAGTTCGATATTTATGTAATGAATGACTATTAACTTACACA 612
QY 119 GluLysArgPheThrMetArgPheArgArgGlyLysAsn---HisSerTyrPheHisAsp 137	119	GluLysArgPheThrMetArgPheArgArgGlyLysAsn---HisSerTyrPheHisAsp 137

Db 613 CTACTGAAATTACACCTGGCTATCAAGATTAATATGTAAGCAAAAAATTTGAGCAA 672  
 Oy 138 LeuValPhe--AsnLeuLeuGluLysAsnValThrArgAspAlaAspAlaThrAspIle 156  
 Db 673 TTAACTTTTGGCTACAGAACTAGTTCAAAAAGTAAAAAGATGGCTCTCCGCAAGATATT 732  
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 Db 793 GGTTTGAATTATCTTAATACATTCACGATGTAAATGTAGAGAAATTAATTTATTCGGG 852  
 Oy 197 ---TrrpGlyLeuValAlaLeuLysGlnIleLeuArgSerAsnLeuProLeu----- 213  
 Db 853 CGTTCACCTTTAAAACTGCATCGAAATTAATTAATAAGAAAAATGTCAAAAACAAGTGGC 912  
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 Db 1087 CCTACA-----CTTCTTAATACCTTTTCTTAATCTTAATTAATTAAGTAAAGCA 1137  
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 Oy 348 -----LysAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsn 364  
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 Oy 385 -----LeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnAsnGluIle 402  
 Db 1309 AAATTATTTGCCAGATCAATCTGGACAA-----ATCTATTAATCAAAATTAACATA 1359  
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RESULT 39  
 US-08-471-046A-31  
 : Sequence 31, Application US/08471046A  
 : Patent No. 5866326  
 : GENERAL INFORMATION:  
 : APPLICANT: Warren, Gregory W  
 : APPLICANT: Kozien, Michael G  
 : APPLICANT: Mullins, Martha A  
 : APPLICANT: Nye, Gordon J  
 : APPLICANT: Cair, Brian  
 : APPLICANT: Desai, Nalini M  
 : APPLICANT: Kostichka, N. Kristy  
 : APPLICANT: Duck, Nicholas B  
 : APPLICANT: Estruch, Juan J  
 : TITLE OF INVENTION: Method For Isolating Vegetative Insecticidal  
 : TITLE OF INVENTION: Protein Genes  
 : NUMBER OF SEQUENCES: 50  
 : CORRESPONDENCE ADDRESSES:  
 : ADDRESS: No. 5866326artis Corporation  
 : STREET: 3054 Cornwallis Road  
 : CITY: Research Triangle Park  
 : STATE: NC  
 : COUNTRY: USA  
 : ZIP: 27709  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patent Release #1.0, Version #1.308  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/471,046A  
 : FILING DATE: 06-JUN-1995  
 : CLASSIFICATION: 435  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 08/463,483  
 : FILING DATE: 05-JUN-1995  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 08/314,594  
 : FILING DATE: 09-SEP-1994  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 08/218,018  
 : FILING DATE: 23-MAR-1994  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 08/037,057  
 : FILING DATE: 25-MAR-1993  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Meigs, J. Timothy  
 : REGISTRATION NUMBER: 38,241  
 : REFERENCE/DOCKET NUMBER: CGC1695/CIP3/DIV8 - SOLv4  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 919-541-8587  
 : TELEFAX: 919-541-8689  
 : INFORMATION FOR SEQ ID NO: 31:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 2612 base pairs  
 : TYPE: nucleic acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
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 : NAME/KEY: CDS  
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 : OTHER INFORMATION: /note= "Native DNA sequence  
 : OTHER INFORMATION: encoding VIP3a(b) from AB424"  
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 : Alignment Scores:  
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 : Score: 96.50 Matches: 102  
 : Percent Similarity: 36.18% Conservative: 80  
 : Best Local Similarity: 20.28% Mismatches: 202

Query Match:	4.09%	Indels:	119
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QY 4 SeraspSerValGlaSPValThrLysThrLeuLeuAlaAlaSerGluSerValAspSer 23	:     :		
DB 235 ACGGATACAGGTGGTGCATCAAC-----CTACACGA 267	:     :		
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DB 328 AGCTTAATGATCTTATTCGACAG-----GGAACCTTAATACAGATT 372	:     :		
QY 64 SerAlaTyrMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSerLeuLysTyr 83	:     :		
DB 373 TCTAAGAAATATTTAAATAATTCGAAATGAAATCAAGTTTAAATGATGTTATATAC 432	:     :		
QY 84 ProLeuGluAla-----LysTyrGlnPro----- 91	:     :		
DB 433 AAATCCGATGGCATTAATACGATGCTTCGGGTATATCTACTAAATTAACCTCTATG 492	:     :		
QY 92 -----LeuThrLeuProAspProTyr-----Gln 99	:     :		
DB 493 AGTGATGTAAAGAAACAAATTTATGCCCTTAAGCTCCAAATAGAAATCTTAAGTAACAA 552	:     :		
QY 100 LeuGluAlaAlaPheIleLeuPheLysGluSerAspAlaAsnPro---AlaAsnSerThr 118	:     :		
DB 553 TTGCAAGAGATTTCTGCATTAAGTTGCATATTATTAAATGTAATATGACTTATTACTATCA 612	:     :		
QY 119 GluLysArgPheTyrMetArgPheArgArgGlyLysAsn---HisSerTyrPheHisAsp 137	:     :		
DB 613 CTTAAGTAATTAACACCTCGGTATCAAGAGATTAAATATGTGAACAAATAATTTGAGAA 672	:     :		
QY 138 LeuValPhe---AsnLeuLeuGluLysAsnValThrArgAspAlaSerAlaThrAspIle 156	:     :		
DB 673 TTAACCTTTGCTACAGAAACTAGTTCAAAAGATTAATAAAGATGGCTCTCGTCAAGATT 732	:     :		
QY 157 GluAsnPhelaIleSerArgTyrLeuTyrMetAlaThrLeuTyrTyrLysThrTyrHisn 176	:     :		
DB 723 CGTGATGAGTTAACTGAGTTAACTGAGCACTAGCAAAAGTGAACAAATAATGATGGAT 792	:     :		
QY 177 ValAspGluPheGlyAlaSerPhePheAsnLysLeuSerPheThrThrGlyLeuPheGly 196	:     :		
DB 793 GGTTTTGAAATTTTCTTAATACATTCACAGAGCTAATGGTAGAAATTAATTAATTCGGG 852	:     :		
QY 197 ---TrpGlyIleLysArgAlaLeuLysGlnIleIleArgSerAsnLeuProLeu----- 213	:     :		
DB 853 CGTTCAGCTTTAAAAACTGCATCGGAATTAACTTACAAAGAAATGTGAACAAACAGTGC 912	:     :		
QY 214 ---AspIleGlyThrGlnHisSer-----ValSerArgLeuGlnHisIleThr 228	:     :		
DB 913 AGTGAGTCGGAATAATGTTTAACTTCCTAATGTGTAAACAGCTCGCA----- 963	:     :		
QY 229 SerSerTyrLysAspTyrMetAspThrGlnIleProAlaLeuProLysPheAlaLysArg 248	:     :		
DB 964 -----GCAAAAGCT 972	:     :		
QY 249 PheSerLeuMetValValGlnArgLeuLeuAlaThrValAlaGlyTyrValAspThrPro 268	:     :		
DB 973 TTTCTTACTTTAAACACATCGCGAAATTTATAGGCTTAGACAGATTTGATATTACTTCT 1033	:     :		
QY 269 TrpTyrLysLysTrpTyrMetLysLeuLys---AsnPheMetValAsnArgValPheIle 287	:     :		
DB 1033 ATTATGAATGACAACTTTAAATAGGAAGAAAGAGCAATTTAGAGTAAAC-----ATCCTC 1086	:     :		
QY 288 ProThrLysLysPhePheAsnLysGluIleArgGluProSerLysAlaLeuLysGluLys 307	:     :		
DB 1087 CCAACA-----CTTTCTAATACTTTTCTTAATCTTAATTAATTAATCAAAAGTTAAAGCA 1137	:     :		

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OY 308 valserthrapsrhrlysaapleupheglnuanslyslleclglnclgltYthrValasphelleasn 327
Db 1138 AGTGATGAAGATGCGAAGATGATTGTGGAGGCTAAACCGACATGCATGATCTTGGGTTT 1197
OY 328 pheasnlysguilearGaasproserlysaLaLeuLySglulysValserasnaspala 347
Db 1198 -----lysAspleupheglnuanslyslleclglnclgltYthrValasphelleasn 364
OY 348 -----lysAspleupheglnuanslyslleclglnclgltYthrValasphelleasn 364
Db 1216 ATTCAGATATTAAAGATATGAGGCTAGCTAAACAA-----AAT 1257
OY 365 AsnGuilearGaasproserlysaLaLeuilearLySValserThrclYalagluasp 384
Db 1258 TATCAAGTC-----GATTAAGGATTCCTTATCGAAGTATTATTATGCGATATGAT 1308
OY 385 -----LeupheguanslyslleclglnclgltYthrValasphelleasnsluile 402
Db 1309 AAATATTATTGCCCCAGATCAATCTGCACA-----ATCTATTATTAACAATTAACATA 1358
OY 403 ArgAspproserlysaLaLeuilearLySVal----- 413
Db 1360 GTATTTCGAATGAATATGTAATTACTAAAAATGATTCTCACTAAAAAATGAACCTTGA 1419
OY 414 ---TyrThrGluAlaAspAspleupheglnuanslyslleclglnclgltYthrValasphe 432
Db 1420 AGAATATGAGGTAAACGCAATTTTATGATCTCTTCAAGGAGAA-----ATTAC-- 1470
OY 433 ileasnlysguilearGaasproserlysaLaLeuilearLySValserThrGluAla 452
Db 1471 TTTAAATTAAGAAAAGATAGCAATCAAGTGAAGCGGATATAGAACGTTAAGTCTAATGAT 1530
OY 453 Aspasnleu 455
Db 1531 GATGGGGTG 1539

RESULT 40
US-08-470-566B-31
; Sequence 31, Application US/08470566B
; Patent No. 5872212
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Koziele, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalin M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: No. 5872212zel Pesticidal Proteins and Strains
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5872212artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,566B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/463,483
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA: US 08/314,594
; APPLICATION NUMBER:

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